

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 14:29:37 ; Search time 12078 Seconds  
(without alignments)  
12967.970 Million cell updates/sec

Title: US-09-697-898-1

Perfect score: 5245

Sequence: 1 gagaaatggcgggcgggc.....tttcaaaccaaaaaaaaaa 5245

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estinv.\*

4: em\_estmus.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_hct.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_hct.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rtd.\*

26: em\_gss\_phg.\*

27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID       | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| 1          | 843.4 | 16.1        | 893    | 13 BUI72741 | BUI72741 AGENCOURT |
| 2          | 787.8 | 15.0        | 836    | 9 AUI32367  | AUI32367 AUI32367  |
| 3          | 738.8 | 14.1        | 835    | 13 BUI94120 | BUI94120 AGENCOURT |
| 4          | 682.4 | 13.0        | 1043   | 12 BM928438 | BM928438 AGENCOURT |

|    |       |      |     |    |          |
|----|-------|------|-----|----|----------|
| 5  | 601   | 11.5 | 949 | 14 | CF409553 |
| 6  | 598   | 11.4 | 653 | 9  | AL042445 |
| 7  | 583   | 11.1 | 868 | 12 | BI654958 |
| 8  | 546.8 | 10.4 | 799 | 14 | CA512935 |
| 9  | 544   | 10.4 | 716 | 9  | AJ450706 |
| 10 | 519.8 | 9.9  | 530 | 10 | AW499603 |
| 11 | 518.8 | 9.9  | 526 | 14 | CF143161 |
| 12 | 514   | 9.8  | 752 | 14 | CA512956 |
| 13 | 504   | 9.6  | 719 | 12 | BI655574 |
| 14 | 500.8 | 9.5  | 773 | 14 | CF287689 |
| 15 | 497.4 | 9.5  | 499 | 13 | BA485112 |
| 16 | 495.4 | 9.4  | 642 | 10 | BE162514 |
| 17 | 494.2 | 9.4  | 714 | 10 | BE981914 |
| 18 | 485.6 | 9.3  | 624 | 10 | AW916314 |
| 19 | 484.6 | 9.2  | 696 | 14 | CF519921 |
| 20 | 484.2 | 9.2  | 714 | 10 | BE981478 |
| 21 | 479.6 | 9.1  | 486 | 12 | BM148300 |
| 22 | 476.4 | 9.1  | 768 | 9  | AJ442678 |
| 23 | 473   | 9.0  | 473 | 9  | AI538525 |
| 24 | 472   | 9.0  | 472 | 13 | AX095560 |
| 25 | 470   | 9.0  | 470 | 9  | AL135609 |
| 26 | 470   | 9.0  | 476 | 10 | AW502619 |
| 27 | 458.4 | 8.7  | 830 | 14 | CB559647 |
| 28 | 457.6 | 8.7  | 870 | 13 | BUI11215 |
| 29 | 455.2 | 8.7  | 460 | 10 | BE242824 |
| 30 | 451.2 | 8.6  | 834 | 14 | CF409554 |
| 31 | 448.2 | 8.5  | 881 | 13 | BU904431 |
| 32 | 445.6 | 8.5  | 452 | 9  | AI684800 |
| 33 | 443.4 | 8.5  | 592 | 13 | BQ830084 |
| 34 | 439.8 | 8.4  | 492 | 10 | AW580454 |
| 35 | 434.8 | 8.3  | 511 | 10 | BF465762 |
| 36 | 431.8 | 8.2  | 595 | 10 | BE956678 |
| 37 | 411.2 | 7.8  | 431 | 14 | CF143770 |
| 38 | 408.8 | 7.7  | 420 | 10 | AW501166 |
| 39 | 403.4 | 7.7  | 903 | 13 | BQ430775 |
| 40 | 397.2 | 7.6  | 556 | 10 | BE853080 |
| 41 | 386.8 | 7.4  | 502 | 29 | CG672158 |
| 42 | 385.4 | 7.3  | 405 | 10 | BF086951 |
| 43 | 381   | 7.2  | 456 | 12 | BI343321 |
| 44 | 380   | 7.2  | 552 | 10 | BF466352 |
| 45 | 379.4 | 7.2  | 670 | 13 | BY748459 |

#### ALIGNMENTS

RESULT 1  
BUI72741  
LOCUS BUI72741 893 bp mRNA linear EST 04-SEP-2002  
DEFINITION AGENCOURT 7964791 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6169242  
5' RNA sequence.  
ACCESSION BUI72741  
VERSION BUI72741.1 GI:226866725  
KEYWORDS EST.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 893)  
NIH-MGC <http://mgc.nci.nih.gov/>  
National Institutes of Health  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DTF  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1AM13534 row: a column: 19  
High quality sequence stop: 671.

[illegible]

QY 4311 TGGCTGCTATTATAGAAATGGCTTGTGCAAAACCAACCAATGGAATGCAGAAAAACACTC 4370  
Db 301 TGGCTGCTATTATAGAAATGGCTTGTGCAAAACCAACCAATGGAATGCAGAAAAACACTC 360  
QY 4371 CAATCACTGCTCTTGTATTTATAGATTTGCTAGTGCACACTGCTCTCATCGATCCCTTC 4430  
Db 361 CAATCACTGCTCTTGTATTTATAGATTTGCTAGTGCACACTGCTCTCATCGATCCCTTC 420  
QY 4431 ACATTTGCTCTCTGTTTACAGATGCTGCTCTTGTGTTTGAAGATTTCAACCTCAGGA 4490  
Db 421 ACATTTGCTCTCTGTTTACAGATGCTGCTCTTGTGTTTGAAGATTTCAACCTCAGGA 480  
QY 4491 CAGACCTCCATCAGAGAGCTACTGAGCAGCTCAGTCTTTCGCTACTACATGCTAGCCAT 4550  
Db 481 CAGACCTCCATCAGAGAGCTACTGAGCAGCTCAGTCTTTCGCTACTACATGCTAGCCAT 540  
QY 4551 TATGCAGATCAACTACAGTGAAGAACAGATGCTCAACAGAGAAAAAACTTTGTGGGA 4610  
Db 541 TATGCAGATCAACTACAGTGAAGAACAGATGCTCAACAGAGAAAAAACTTTGTGGGA 600  
QY 4611 ACCACATTTGATTTCTACTGCTCCATGATGCCACTGACAGCTATGACAGGCGCAGTGG 4670  
Db 601 ACCACATTTGATTTCTACTGCTCCATGATGCCACTGACAGCTATGACAGGCGCAGTGG 660  
QY 4671 GAAACCTTTACCTAAGTATGTTGATTCACAAATCATGATCTGTACCTAAGCTCAGTATCAA 4730  
Db 661 GAAACCTTTACCTAAGTATGTTGATTCACAAATCATGATCTGT-CCTAAGCTCAGTATCAA 719  
QY 4731 AAGCCCAAACTAGTGCAGAACTGTAACTGTGCTTTCAAGAACTGGCCCTAGGTGAA 4790  
Db 720 AAGCCCAAACTAGTGCAG-AACTGTAACTGTGCTTTCAAGAACTGGCCCTAGGTGAA 778  
QY 4791 CAGGAAAAAATGAAGTTTGATGCTGATGCTAAATTCAGAGAGATAATTTATTTTGGGA 4849  
Db 779 CAGG-AAAACATGAATTTTCATGATGCTAAATTCAGAGAGATAATTTATTTTGGGA 836

## RESULT 3

BU194120 895 bp mRNA linear EST 04-SEP-2002  
LOCUS AGENCOURT\_7968818 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6148258  
5', mRNA sequence.

ACCESSION BU194120

VERSION BU194120.1 GI:22708104

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 895)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: ATCC/DCTP/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

Cloning Distribution: Agencourt Bioscience Corporation

Cloning Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLN at:

<http://image.llnl.gov>

Plate: LLM13479 row: g column: 11

High quality sequence stop: 688.

Location/Qualifiers

1..895

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6148258"

/tissue\_type="melanotic melanoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_72"

## FEATURES

source

/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 2 kb. Library constructed by Life  
Technologies."

## ORIGIN

Query Match 14.1%; Score 738.8; DB 13; Length 895;  
Best Local Similarity 98.5%; Pred. No. 2.6e-118;  
Matches 767; Conservative 0; Mismatches 8; Indels 4; Gaps 2;  
QY 3599 CTGAGATGCCCTCCCATAGTTCCTCAGCTGCAGTGTGAAATGAGAGATATCATCA 3658  
Db 53 CGCAGATGCCCTCCCATAGTTCCTCAGCTGCAGTGTGAAATGAGAGATATCATCA 112  
QY 3659 TTATTCAACAGATACACAGAGACTCTACAGGACATACCAAGCAAAACACCGTATA 3718  
Db 113 TTATTCAACAGATACACAGAGACTCTACAGGACATACCAAGCAAAACACCGTATA 172  
QY 3719 GAGAAGACACTGAATGGCTGAAAGGTCAACAGATAGGCTTGGAGCATTTTCTTCTGTT 3778  
Db 173 GAGAGACACTGAATGGCTGAAAGGTCAACAGATAGGCTTGGAGCATTTTCTTCTGTT 232  
QY 3779 ATCAGGCTCAAGATGTGGAACTGGAACCTTTAATGGCTGTTAAACAGGTGACTTATGCA 3838  
Db 233 ATCAGGCTCAAGATGTGGAACTGGAACCTTTAATGGCTGTTAAACAGGTGACTTATGCA 292  
QY 3839 GAAACACATCTTCTGAGCAAGAGAGAGTAGTAGAGCACTAAGAGAGAGATAAGAAATGA 3898  
Db 293 GAAACACATCTTCTGAGCAAGAGAGAGTAGTAGAGCACTAAGAGAGAGATAAGAAATGA 352  
QY 3899 TGAGCCATCTGAATCATCCAAACATCATTTAGGATGTGGAGCCACGCTGTGAGAGAGCA 3958  
Db 353 TGAGCCATCTGAATCATCCAAACATCATTTAGGATGTGGAGCCACGCTGTGAGAGAGCA 412  
QY 3959 ATTACATCTCTTCAATGATGGAGGGGGATCGTGGCTCATTTGCTGAGTAAT 4018  
Db 413 ATTACATCTCTTCAATGATGGAGGGGGATCGTGGCTCATTTGCTGAGTAAT 472  
QY 4019 ATGGAGCCCTTCAAGAAATCAGTAGTTATTAATACACTGAACAGATTACTCCGTGGCCTTT 4078  
Db 473 ATGGAGCCCTTCAAGAAATCAGTAGTTATTAATACACTGAACAGATTACTCCGTGGCCTTT 532  
QY 4079 CGTATCTCCATGAAACCAATCATTCACAGAGATGTCAAGGTGCCAATTTGCTAATTG 4138  
Db 533 CGTATCTCCATGAAACCAATCATTCACAGAGATGTCAAGGTGCCAATTTGCTAATTG 592  
QY 4139 ACAGCACTGGTCAGAGACTAAGAATTCAGATTTTGGAGCTGCAGCCAGTTGGCATCAA 4198  
Db 593 ACAGCACTGGTCAGAGACTAAGAATTCAGATTTTGGAGCTGCAGCCAGTTGGCATCAA 652  
QY 4199 AAGGAACTGGTCAGAGAGAGTTTCAGGGACAATTTACTGGGGACAATTTGCAATTATGGCAC 4258  
Db 653 AAGGAACTGGTCAGAGAGAGTTTCAGGGACAATTTACTGGGGACAATTTGCAATTATGGCAC 712  
QY 4259 CTGAGGTACTAAGAGGTCAACAGTATGGAAGGAGCTGTGATGTATGGAGTGT-TGGCTGT 4317  
Db 713 CTGAGGTACTAAGAGGTCAACAGTATGGAAGGAGCTGTGATGTATGGAGTGT-TGGCTGT 772  
QY 4318 GCTATTATAGAAATGGCTTGTGCAAAACCAACCC---ATGGAATGCAAGAAAAACACTCCAA 4373  
Db 773 GCTATTATAGAAATGGCTTGTGCAAAACCAACCCATGGGNAATGCAAGAAAAACACTCCCA 831

## RESULT 4

BM928438

LOCUS

DEFINITION

5', mRNA sequence.

ACCESSION

BM928438

VERSION

BM928438.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

BM928438 1043 bp mRNA linear EST 12-MAR-2002  
AGENCOURT\_6699830 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5770238  
5', mRNA sequence.

ACCESSION

BM928438

VERSION

BM928438.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1043)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

Tissue procurement: Life Technologies, Inc.

cDNA library preparation: Life Technologies, Inc.

cDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12832 row: p column: 15

High quality sequence stop: 625.

Location/Qualifiers

1..1043

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5770238"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_121"

/note="Organ: Brain; Vector: pCMV-Sport6; Site\_1: NotI;

Site\_2: EcoRV (destroyed); RNA source anonymous pool of 3

fetal brains, female age 20 weeks, female age 24 weeks,

and male age 26 weeks. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range

0.7-3.5 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 017. Note:

this is a NIH\_MGC Library."

## ORIGIN

Query Match 13.0%; Score 682.4; DB 12; Length 1043;

Best Local Similarity 99.0%; Pred. No. 1.8e-108;

Matches 697; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 4541 GGTAGCAATTATGCAATCACTACAGTAGAAGAGGATGCTAACAGAGAAAAAAA 4600

DB 1 GGTAGCAATTATGCAATCACTACAGTAGAAGAGGATGCTAACAGAGAAAAAAA 60

QY 4601 CTT-GTGGGAACCACTATGATTTCTACTGGCCATGATGCCACTGAACAGCTATGAACG 4659

DB 61 CTTGGTGGGAACCACTATGATTTCTACTGGCCATGATGCCACTGAACAGCTATGAACG 120

QY 4660 AGCCAGTGGGAACCCCTTACCTACCTAGTATGTGATGACAAATCATGCTGTACCTAAGC 4719

DB 121 AGCCAGTGGGAACCCCTTACCTACCTAGTATGTGATGACAAATCATGCTGTACCTAAGC 180

QY 4720 TCAGTATGCAAAAGCCCAACTAGTCAGAACTGTAACTGTGCTTTCAAGAACTGG 4779

DB 181 TCAGTATGCAAAAGCCCAACTAGTCAGAACTGTAACTGTGCTTTCAAGAACTGG 240

QY 4780 CCCTAGTGAACAGGAAAAACAATGAAGTTTGCATGACTAAATTCGACAGCAATATTTTA 4839

DB 241 CCCTAGTGAACAGGAAAAACAATGAAGTTTGCATGACTAAATTCGACAGCAATATTTTA 300

QY 4840 TTTTGTGGAGCACTTTTTCAGCAATATTAGCGGCTCAGGCTCAGGATCTATTTAAT 4899

DB 301 TTTTGTGGAGCACTTTTTCAGCAATATTAGCGGCTCAGGCTCAGGATCTATTTAAT 360

QY 4900 ATTTCAATTAATTTTCCATTTTCATATAGTGATCACAAGCAGGCGGTCTGCAATTCGGT 4959

DB 361 ATTTCAATTAATTTTCCATTTTCATATAGTGATCACAAGCAGGCGGTCTGCAATTCGGT 420

QY 4960 CAAATTTTGTCACTGGCTATAAAATCAGTATCTGCCTCTTTTAGGTGAGTAGTGTCTA 5019

DB 421 CAAATTTTGTCACTGGCTATAAAATCAGTATCTGCCTCTTTTAGGTGAGTAGTGTCTA 480

QY 5020 TGAGTAGCAATACATACATATATTTTAAAGTGTGACTTCTTTATGACCCACAGTTGA 5079

DB 481 TGAGTAGCAATACATACATATATTTTAAAGTGTGACTTCTTTATGACCCACAGTTGA 540

QY 5080 CCTTATTTTCTTAATACACAGGAGTGTGGCTCATGTGCAATTTACTGTTGGCCCA 5139

DB 541 CCTTATTTTCTTAATACACAGGAGTGTGGCTCATGTGCAATTTACTGTTGGCCCA 600

QY 5140 TTCATTTTCGTTTTTGGAAATATGTTTTGTATTTTTCATGTTTTTATTTACATTTTG 5199

DB 601 TTCATTTTCGTTTTTGGAAATATGTTTTGTATTTTTCATGTTTTTATTTACATTTTG 660

QY 5200 TTTATTCAGGAAAGCTGATCTTTTTTTCACACCAAAAAAAA 5243

DB 661 TTTATTCAGGAAAGCTGATCTTTTTTTCACACCAAAAAAAA 704

## FEATURES

source

CF409553 949 bp mRNA linear EST 02-SEP-2003

CH3#061\_D05MF Canine heart normalized cDNA Library in pBluescript

Canis familiaris cDNA clone CH3#061\_D05 5', mRNA sequence.

CF409553

CF409553.1 GI:34410799

KEYWORDS

EST.

SOURCE

ORGANISM

Canis familiaris (dog)

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 949)

Yi, Y., Desai, R., Olarte, M., Henthorn, P. and George A.L.

Expressed sequence tags from Canine heart

Unpublished (2003)

Other ESTs: CH3#061\_D05ME

Contact: George AL

Division of Genetic Medicine

Vanderbilt University

529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA

Tel: 615 936 2660

Fax: 615 936 2661

Email: [al.george@vanderbilt.edu](mailto:al.george@vanderbilt.edu)

Insert length: 1552 Std Error: 0.00

Seq primer: MF: GTTTCCTCCAGTCACGACGTTG

High quality sequence start: 165

High quality sequence stop: 780.

FEATURES

source

1..949

/organism="Canis familiaris"

/mol\_type="mRNA"

/db\_xref="taxon:9615"

/clone="CH3#061\_D05"

/tissue\_type="heart"

/cell\_type="heart"

/dev\_stage="mixed developmental stages (adult, 30 day - 40

day fetal)"

/clone\_lib="Canine heart normalized cDNA Library in

pBluescript"

/note="Organ: heart; Vector: pBluescript; Site\_1: 5' of

vector NotI; Site\_2: 3' of vector EcoRI; Tissue source:

dog heart (adult, 30 day - 40 day fetal), right and left

atria and ventricle. Dog breed - mixed (beagle, German

shepherd, pointer, Irish setter). Library construction:

oligo-dT primed"

## ORIGIN

Query Match 11.5%; Score 601; DB 14; Length 949;

Best Local Similarity 92.6%; Pred. No. 2.7e-94;

Matches 653; Conservative 0; Mismatches 50; Indels 2; Gaps 2;

QY 4069 CGTGGCTTTTGGTATCTCCATGAACCAATATCATTCACAGAGATGTCAAAGTGCCAAT 4128

DB 165 CGTGGCTTTTGGTATCTCCATGAACCAATATCATTCACAGAGATGTCAAAGTGCCAAT 224



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QY 4129 TTGCTAAATTGACAGCACTGGTCAGAGACTAAGAAATTGAGATTTTGGAGCTGCAGCCAGG 4188
Db 225 TTGCTAAATTGACAGCACTGGTCAGAGACTGAGAAATTGAGATTTTGGAGCTGCAGCCAGG 284
QY 4189 TTGGCATCAAAAGGAACCTGGTCAGAGAGTTTCAGGACAAATTACTTGGGACAAATTGCA 4248
Db 285 TTGGCATCAAAAGGAACCTGGTCAGAGAGTTTCAGGACAAATTACTTGGGACAAATTGCA 344
QY 4249 TTTATGGCACTGGAGTACTAAGAGGTCACAGTAGTGAAGAGGAGCTGTGATGTATGGAGT 4308
Db 345 TTTATGGCACTGGAGTACTGAGAGGTCAGAGTAGTGAAGAGGAGCTGTGATGTATGGAGT 404
QY 4309 GTTGGCTGTGCTATTATAGAAATGCTTGTGCAAAACCAACCATGAGATGCAAGAAACAC 4368
Db 405 GTTGGCTGTGCTATTATAGAAATGCTTGTGCAAAACCAACCATGAGATGCAAGAAACAC 464
QY 4369 TCCATATCTTGTCTTTGATATTTAAGATTTGCTAGTCAACTACTGCTCCCATCGATCCCT 4428
Db 465 TCCATATCTTGTCTTTGATATTTAAGATTTGCAAGTGGAGGAGCTGCTCCATCAATCCCC 524
QY 4429 TCACATTTGTCTCTGGTTTACAGAGATGAGGCTCTTCTGTTTGTAGAACTTCAACCTCAG 4488
Db 525 TCACATTTGTCTCTGGTTTACAGAGATGAGGCTCTTCTGTTTGTAGAACTTCAACCTCAG 584
QY 4489 GACAGACCTCCATCAAGAGAGCTACTGAAGCATCCAGTCTTTTCTGCTACTACATGTAGCCA 4548
Db 585 GACAGACCTCCATCAAGAGAGCTACTGAAGCATCCAGTCTTTTCTGCTACTACATGTAGCCA 644
QY 4549 ATTATGCAAGTCAACTACAGTAGTAGAAGAGATGCTCAACAGAGAAAAAACTTTGTGGG 4608
Db 645 ATTATGCAAGTCAACTACAGTAGTAGAAGAGATGCTCAACAGAG-CAAAACTTTTGTGGG 703
QY 4609 GAACACATTTGATATTTCTACTGGCCATGATGCTGACAGCTATGACAGGCGCAGTG 4668
Db 704 GAACACATTTGATATTTCTACTGGCCATGATGCTGACAGCTATGACAGGCGCAGTG 763
QY 4669 GGGAAACCTTCACTAAGTATGTGATGCAAAATCATGATCTGTACTAAGCTCACTATGC 4728
Db 764 GGGAAACCTTCACTAAGTATGTGATGCAAAATCATGATCTGTACTAAGCTCACTATGC 823
QY 4729 AAAAGCCCA-ACCTAGTGCAGAACTGTAAACTGTGCTTCAAA 4772
Db 824 CAAAGTCCCAATTTGTGCACAACTGTAAACCGTGCCTTTCAAA 868

RESULT 6
AL042445 653 bp mRNA linear EST 04-SEP-2003
DEFINITION DKF2p434D2221_r1 434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION AL042445
VERSION AL042445.1 GI:5421814
KEYWORDS EST.
SOURCE EST (Blum, et al.)
ORGANISM Homo sapiens (human)
REFERENCE Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
AUTHORS Blum, H., Bauer-Sachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (bases 1 to 653)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
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FEATURES
source 1..653
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2p434D2221"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match 11.4%; Score 598; DB 9; Length 653;
Best Local Similarity 98.6%; Pred. No. 8.8e-94;
Matches 624; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

QY 3856 CAGAGAGAGTAGTAGAAGCACTAGAGAGAGAGATGATGAGCCATCTGATCAT 3915
Db 1 CAAGAGAGAGTAGTAGAAGCACTAGAGAGAGATGATGAGCCATCTGATCAT 60
QY 3916 CCAACATCATTTAGGATGTTGGAGCCACGTGTGAGAGAGCAATTTCAATCTCTTCAAT 3975
Db 61 CCAACATCATTTAGGATGTTGGAGCCACGTGTGAGAGAGCAATTTCAATCTCTTCAAT 120
QY 3976 GAATGATGCGAGGGGATGCGTGGCTCATTTGCTGAGTAAATATGAGGCTTCAAGAA 4035
Db 121 GAATGATGCGAGGGGATGCGTGGCTCATTTGCTGAGTAAATATGAGGCTTCAAGAA 180
QY 4036 TCAGTAGTTATTAACTACACTGAACAGTACTACCTGGGCTTTTCGTATCTCCATGAAAC 4095
Db 181 TCAGTAGTTATTAACTACACTGAACAGTACTACCTGGGCTTTTCGTATCTCCATGAAAC 240
QY 4096 CAAATCATTTACAGAGATGTCAGAGTGCATTTGCTTAATTCAGAGCTGTGAGAGA 4155
Db 241 CAAATCATTTACAGAGATGTCAGAGTGCATTTGCTTAATTCAGAGCTGTGAGAGA 300
QY 4156 CTAAGAAATTCAGATTTTGGAGCTGCAGCAGGTTGCGATCAAAAGGAACTGTCGAGGA 4215
Db 301 CTAAGAAATTCAGATTTTGGAGCTGCAGCAGGTTGCGATCAAAAGGAACTGTCGAGGA 360
QY 4216 GAGTTTCAGGAGCAATTTACTTGGGACAATTTGCAATTTATGGACCTGAGGTAAGAGGT 4275
Db 361 GAGTTTCAGGAGCAATTTACTTGGGACAATTTGCAATTTATGGACCTGAGGTAAGAGGT 420
QY 4276 CAACAGTATGGAAGGAGCTGTGATGATGAGGTTTGGCTGTCTATTATAGAAATGGCT 4335
Db 421 CAACAGTATGGAAGGAGCTGTGATGATGAGGTTTGGCTGTCTATTATAGAAATGGCT 480
QY 4336 TGTGCAAAACCACTCATGGAATGCAGAAAAACACTCCAATCATCTTCTTTGATATTAAAG 4395
Db 481 TGTGCAAAACCACTCATGGAATGCAGAAAAACACTCCAATCATCTTCTTTGATATTAAAG 540
QY 4396 ATTGCTAGTGCACACTACTGCTCCATCGATCCCTTCACATTTGCTGCTGTTTACGA--G 4453
Db 541 ATTGCTAGTGCACACTACTGCTCCATCGATCCCTTCACATTTGCTGCTGTTTACGAAGA 600
QY 4454 ATGTGGCTCTTCTGTTGTTT-AGAATTTCAACCT 4485
Db 601 TGTGGCTCTTCTGTTGTTT-AGAATTTCAACCT 633

RESULT 7
BI654958 868 bp mRNA linear EST 12-SEP-2001
LOCUS 603283220F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5327644 5',
DEFINITION mRNA sequence.
ACCESSION BI654958
VERSION BI654958.1 GI:15569194
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 868)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth

Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11831 row: g column: 05

High quality sequence stop: 821.

Location/Qualifiers

1..868

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="NMRI"

/db\_xref="taxon:10090"

/clone="IMAGE:5327644"

/tissue\_type="tumor, gross tissue"

/dev\_stage="5 months"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP Mam4"

/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Priscilla Furth,

NIH Reference for transgenic model: Li et al., Cell Growth

and Differentiation 7, 3-11 (1996)."

ORIGIN

Query Match 11.1%; Score 583; DB 12; Length 868;

Best Local Similarity 85.0%; Pred. No. 3.6e-91;

Matches 664; Conservative 0; Mismatches 115; Indels 2; Gaps 1;

483 CGCGGTCGTGAGATGAGGAGAACTCTCAAGGGTTGCACAGATGATGATCG 542

64 CGCGAATCGAGATGAGGAGAACTCTCAAGGGTTGCACAGATGAGGATCG 123

543 TCCAGAGAACGATGATCGAGGAGAACTGAGGAACTGTATGCCAGCTGGAGCA 602

124 CCGGAGAGAGATGATCGGAGAGAGCTCAGGCGACCTGTATGCCGCTGGAGCA 183

603 CGAATGCTGAGAGGAGAACTGCGAGGCGCTGTGTAAACCAATCCAGTTAA 662

184 CGAGTGGTTGAGAGGAGGAGACAGAGAGGCCCTGTGTGTGAGCAATCCCTATTA 243

663 AGGAGATGGATCTGAATGAATCACTTAGCAGTGTGATCCAGGAGAGTCCAGGCAAG 722

244 AGGAGATGGATCTGAATGAATCACTTAGCAGTGTGATCCAGGAGAGTCCAGGCAAG 303

723 TCGGCTTCACAGCTTCCAAAGCCGAGCGAGTCTCTCTGCGAATCCCATCAGG 782

304 TTCGCTGCACAGCCCCCAGGCGGAGAGCCATCTCTCTGCGAATCTCTGCGAAT 363

783 TCGCACAGTGAATCAGAACTCCAGGAGTGAAGGAGAAAGAGTTTCCCGAGTGCCTTT 842

364 GCGCTCGTGAAGCGGAATCCCGAGGAGTGAAGGAGAAAGAGTGTCCCGGTGCCTTT 423

843 TCAGATGCGAGATCAACACCCCGAGGAGCCCTTCCAGATGGCTTCCACCATTA 902

424 CCAGATGGCAGATCAACACCCCGAGGAGCCCTTCCAGATGGCTTCCACCATTA 483

903 TAGCCCTGAGGAGAAACAAACCGCGGTGTGTAAAGAGTGTGCGGCCAGAGTGTACT 962

484 CAGCCAGAGGAGAGCGAGCGCGGTGTGAACAAAGTGTGAGCCAGGCTGTACTGCT 543

Qy 963 GCAGCAGATAGGCGCTTCTTCTCTGATTTGGAGGAGAGCCAGCAATAAATACCG 1022

Db 544 GCAGCAGATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 603

Qy 1023 GGTGTTTATTTGGGCGCTCAGAACTGAGCTGTGACGTGGAAATTTCTGATTCTGCT 1082

Db 604 GGTGTTTATTTGGGCGCTCAGAACTGAGCTGTGACGTGGAAATTTCTGATTCTGCT 663

Qy 1083 ATTGTGATCTCGGGTGTTCATTAATAGAACCTTCAGACCCCAATGTTATGGAGAAAC 1142

Db 664 GTTTGTCTATCTCGGGTGTTCATTAATAGAACCTTCAGACCCCAATGTTATGGAGAAAC 723

Qy 1143 TTT--AAAGAAATTTGAGGTTGAGAGTTTCTTCAGAAATATCACAGTAGGCGCTAGCTCA 1200

Db 724 TTTTGAAGAAATTTGAGGTTGAGAGTTTCTTCAGAAATATCACAGTAGGCGCTAGCTCG 783

Qy 1201 AGGATCAAGCTCCATCTCGTAACACCATCCAGAGTTTCTTCAGCAGTGTCAATCTCT 1260

Db 784 AGAATCAAGCTCCATCCCGGAACACCATCCAGAGTTGTCTCCGCGCTGGCAATGGT 843

Qy 1261 C 1261

Db 844 C 844

RESULT 8

LOCUS

CA512935

DEFINITION

UI-R-FJ0-cqb-m-19-0-UI.r1 UI-R-FJ0 Rattus norvegicus cDNA clone

ACCESSION

CA512935

VERSION

CA512935.1 GI:25003889

KEYWORDS

EST.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 799)

Bonaldi,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)

Tissue Procurement: Dr. James Lin, University of Iowa

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics ([www.reagen.com](http://www.reagen.com)).

Seq primer: M13 REVERSE.

Location/Qualifiers

1..799

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-FJ0-cqb-m-19-0-UI"

/tissue\_type="embryo"

/dev\_stage="embryo"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-R-FJ0"

/note="Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I;

UI-R-FJ0 is a cDNA library containing the following

tissue(s): rat embryo. The library was constructed

FEATURES  
source

according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTV73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CATCTCTACT. This library was created for the University of Iowa Program for Rat Gene Discovery and Mapping (Val Sheffield, Bento Soares and Tom Casavant)"

## ORIGIN

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Query Match      10.4%; Score 546.8; DB 14; Length 799;
Best Local Similarity 82.1%; Pred. No. 7.3e-85;
Matches 658; Conservative 0; Mismatches 125; Indels 18; Gaps 2;

QY 2729 TAGAGAAAACCTGAAAAGGATTATGTCTACAAAATTGAGTGGCAGTTTCAGAGGACATTT 2788
DB      |||||
QY 2789 CTGAGAGACTGGCCAGCATTTTCAGTAGACCTTCTAGTTCAACACACACACACACAA 2848
DB      |||||
QY 2790 CTGAGAGACTGGCTGGGGTTTCTGTAGGACTTCTAGTT-----CAGCAA 121
QY 2849 CAACAGAGCAACCAAGCCATGTTTCAACAAAAGGCAGACCCACAGTCAGTGTGTA 2908
DB      |||||
QY 122 CAACAGACACCAAGCCACATTTCAACAAAAGGCAGACCCACAGTCAGTGTGTA 181
QY 2909 ACTCCTCTCCCTTATCATCATTCCTCCAAATTAATGTTTCCAGCTTGTCAACCCCTTCT 2968
DB      |||||
QY 182 ACTCCTCTCCCTTGTCTCTCTC---CTCAGTTAATGTTTCCAGCAATATCAGCCCCATGTT 238
QY 2969 CTTCTACCCCATCTGACACGCTGGCATCTCAACAGATGCTCTTAAGCATAGACTTCAGG 3028
DB      |||||
QY 239 CATCTGCCCGCTGTGTCGAGCTGGCTCTGTAAACAGATGCTCTTAAGCATAGACTTCGG 298
QY 3029 GATTTCATCTCCTGAGAAATACCTTTCTGCATCTCTCTCAACACACGCGCAAGTTTCTTCTAC 3088
DB      |||||
QY 299 CGTTTGTCTCCTGTAAATAACCTCTCGCTCTCCCAACACACAGCGCAAGTTTCTCCTAC 358
QY 3089 AATTCCACAGAACTGTCTGAAACAAAGACTCAGATAACTTTTCCCGAGTCTTTTACTC 3148
DB      |||||
QY 359 AGTTCCAGAGGACCTGTCTGAGAACCGAGACTCAGAAAACCTCTCCCGAGTCTTTTACTC 418
QY 3149 AGTCAAGACCCCTTGCCCTCCAGTAACATACACAGGCCAAAGCCATCTAGACCTACCCAG 3208
DB      |||||
QY 419 AGTCGAGACCCCCACCTCTCCAGTAACATACACAGGCCAAAGCCATCTCCGACCCGTTCCGG 478
QY 3209 GTAATACAGTAACAGGAGATCCCTCAAAAATAGCTGACACTTGATCTGACAGTA 3268
DB      |||||
QY 479 GTAGCACAGCAAACTAGGGGATGCCTCAAAAACAGCATGACACTCGACTGAAACAGTG 538
QY 3269 GTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCAATAGTAGTAATGCTGTTATACCCA 3328
DB      |||||
QY 539 CTTCCAGTGTGATGACAGCTTTGGCAGTGGCAGCAACAGTGGCAGCGCGTCAATACCCA 598
QY 3329 GTGAGGAGAGAGTGTTCACCCAGTAGAGGAGAAATGAGATAGTATAGTATGATCAGAGC 3388
DB      |||||
QY 599 GTGAGGAGAGCGCATTCACCCAGCAGAGGCAAGTGCAGGTTAGATGTCAACCCCGAGC 658
QY 3389 TCAACTCCAGTATTGAGGACCTTTTGAAGCATCTATGCTCTCAAGTGTATACACAGTAA 3448
DB      |||||
QY 659 TCACTCCAGTATCGAGACCTTTTGAGAGATCTATGCTCTCAAGTGTACACACAGTCA 718
QY 3449 CTTTAAAGTGAAGTGTCTGCTCTCTCTGAAAAGGCTGAAAATGATGATACCTTACA 3508
DB      |||||
QY 719 CTTTCAAGTGAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 778
QY 3509 AAGATGATGTGAATCATATTC 3529
DB      |||||
QY 779 NAGATGAGCTCATCACATC 799
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## RESULT 9

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AJ450706
LOCUS      AJ450706 riken1 Gallus gallus cDNA clone 26c20r1, mRNA sequence.
DEFINITION linear
ACCESSION AJ450706
VERSION    AJ450706.1 GI:20217927
KEYWORDS   EST.
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE  1 (bases 1 to 716)
            Buerstedde,J.M.
            Gallus gallus bursal lymphocyte EST
            Unpublished (2002)
            Contact: Buerstedde JM
            Cellular Immunology
            Heinrich-Pette-Institute
            Martinstr. 52, 20251 Hamburg, Germany
            Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
            Location/Qualifiers
              1..716
                /organism="Gallus gallus"
                /mol_type="mRNA"
                /db_xref="taxon:9031"
                /clone="26c20r1"
                /cell_type="bursal lymphocyte"
                /dev_stage="2-3 weeks old"
                /clone_lib="riken1"
                /note="CB inbred strain"
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## FEATURES

source

## ORIGIN

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Query Match      10.4%; Score 544; DB 9; Length 716;
Best Local Similarity 85.8%; Pred. No. 2.2e-84;
Matches 615; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

QY 3546 GATGGAAGCTGAAGAAGAGAGCTTTAGCAATTCCTGCAATGGCAATGTCAGCGTCTCAGA 3605
DB      1 GATGGAAGCTGAAGAAGAGAGCTTTAGCTATTCTGCTATGGCAATGTCGATCTCAAGA 60
QY 3606 TGCCCTCCCTAGTTCCTCAGCTCGAGTGAATGAGAGATATCATCATTTATCA 3665
DB      |||||
QY 61 TGCCCTGCAATTAATTCCTCAACTACAGTCAAAATGCTGAGATATCATTAATTATCA 120
QY 3666 ACAGGATACACAGAGACTCTTACCAGGACATACCAAGCAAAACCAACCGTATAGAGAAGA 3725
DB      |||||
QY 121 GCAGGATACACAGAAACTCTGCTGGACATACCAAGCAAAAGCATATTACAGGGAAGA 180
QY 3726 CACTGATGCTGAAAGTCAACAGATAGGCTTCGGACATTTCTTCTGTTATCAGC 3785
DB      |||||
QY 181 TGCAGATGGCTTAAAGGTCAGCAATTTGCTTGGAGCTTTCTCTCTGTTTACAGC 240
QY 3786 TCAAGATGTGGAACTGGAACTTTAATGGCTGTTAAACAGGTGACTTATGTGAGAAACAC 3845
DB      |||||
QY 241 TCAAGATGTAGGAACAGGAGACATTAATGCTGTAACAGGTGACATATGTGAGGAACAC 3900
QY 3846 ATCTTCTGAGCAAGAAGTAGTAGAGCACTAAGAGAGAGATAGAGATAGATAGGCA 3905
DB      |||||
QY 301 ATCATCTGAGCAAGAAGAGGTAGTGGAGCACTAGGGGAGGAAATACCGATGATGATCA 360
QY 3906 TCTGAATCATCCAAACATCATTTAGATGTTGGAGCCACGCTGTGAGAGAGCAATTAACA 3965
DB      |||||
QY 361 TCTAAACCATCTTAATATTTTCGCATGTTGGGTCTCATGTGAGAGAGCACTACAA 420
QY 3966 TCTTTTCATTAATGATGGCAGGGGATCGGTGGCTCATTTTCTGCTGAGTAATATGGAGC 4025
DB      |||||
QY 421 CCTCTTCATTAATGATGGCAGGGGATCAGTTGCTCATTTGTTGAGTAATATCGGAGC 480
QY 4026 CTTCAAGAAATCAGTAGTTATTAACTACACTGAAAGTTACTCCGTCGGCTTTCTCTATCT 4085
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481 CTTCAAGAAATCAGTTATTATTAACACACAGACAACTGTTACGTGGCCCTTTCTTACCT 540  
4086 CCATGAAACCAAAATCATTTACAGAGATGTCAGAGGTGCCAAATTTGCTAATTCAGACAC 4145  
541 CCATGAGATCAGATAATTCATAGAGATGTCAGAGGTGCCAAATTTGCTAATTCAGACAC 600  
4146 TGGTCAGAGACTAGAAATTCAGATTTTGGAGCTGCGAGCCAGGTTGGCATCAAAAGAAC 4205  
601 AGGTATAGATTAAGAAATTCGTGATTTTGGAGCTGCGAGCCAGGTTGGCATCAAAAGAAC 660  
4206 TGGTCAGAGAGATTTTTCAGGACCAATTAATCTGGGACAAATTTGCAATTTATGCACTGA 4262  
661 TGGTCTGGGAGTTTCAAGGACAGTTT-GTTGGGACTATTGCAATTTATGCCCCCGGA 716

RESULT 10  
AW499603  
LOCUS  
DEFINITION  
UI-HF-BPop-ain-b-12-0-UI.r1 NIH\_MGC\_51 Homo sapiens CDNA clone  
IMAGE:3072335 5', mRNA sequence.  
AW499603  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
EST.  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 530)  
NIH-MGC <http://mgi.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: M3 Forward.

FEATURES  
source  
Location/Qualifiers  
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/lab\_host="DH10B (LTI)"  
/clone\_lib="NIH MGC 51"  
/note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(4.4-7.4kb). Directionally cloned. Cells provided by  
Louis M. Staudt, Ph.D. Library preparation by Maria de  
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN  
Query Match 9.9%; Score 519.8; DB 10; Length 530;  
Best Local Similarity 99.6%; Pred.No. 3.7e-80;  
Matches 521; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2268 TCTTGGCCGCTTGTCTTATAGATACAGCTGTTTGGAAATTCCTGCTGAATTTATCC 2327  
8 TCTTGGCCGCTTGTCTTATAGATACAGCTGTTTGGAAATTCCTGCTGAATTTATCC 67  
2328 TCATATTGTCAGTACTGATGTTTCAAGCTGAGCTGCTGTTGAATCAGGTATAGAAGCT 2387  
68 TCATATTGTCAGTACTGATGTTTCAAGCTGAGCTGCTGTTGAATCAGGTATAGAAGCT 127  
2388 GCTGTCCCTCTTAACCTTTCCTTGGAGTCCATGATTAATCCCACTCAATGTTGGCAA 2447

128 GCTGTCCCTCTTAACCTTTCCTTGGAGTCCATTAATTTCCCACTCAATGTTGGCAA 187  
2448 ACTTTCCAGAGAGATCTACTGAGTTCTGGAAGATGGTTACTACAGTACCCCATGTT 2507  
188 ACTTTCCAGAGAGATCTACTGAGTTCTGGAAGATGGTTACTACAGTACCCCATGTT 247  
2508 TTCAAAACCTGTTAGAAATGCTGAGTTTCCAGTTTCCACTCACTTCCAGGATGCGTGC 2567  
248 TTCAAAACCTGTTAGAAATGCTGAGTTTCCAGTTTCCACTCACTTCCAGGATGCGTGC 307  
2568 CGGTTGATGGCTATGTCAGATGAGTGGAAATTCGCGAGCCATCCAGTTGGGCGTAGA 2627  
308 CGGTTGATGGCTATGTCAGATGAGTGGAAATTCGCGAGCCATCCAGTTGGGCGTAGA 367  
2628 AGACACTTTGGATGCTCAACAGGACAGCTTCTTGAGGAGCATCTGTTCCCAACAATACT 2687  
368 AGACACTTTGGATGCTCAACAGGACAGCTTCTTGAGGAGCATCTGTTCCCAACAATACT 427  
2688 GGAACCCACAGAGACAGTTCCTGAGTGACAGTCCATTTAGAGAAAACCTGGAAGG 2747  
428 GGAACCCACAGAGACAGTTCCTGAGTGACAGTCCATTTAGAGAAAACCTGGAAGG 487  
2748 ATTATGCTCTACAAATTTGAGTGCCAGTTTCAGAGGACATTTCT 2790  
488 ATTATGCTCTACAAATTTGAGTGCCAGTTTCAGAGGACATTTCT 530

RESULT 11  
CF143161  
LOCUS  
DEFINITION  
UI-HF-BPop-ags-f-01-0-UI.r1 NIH\_MGC\_52 Homo sapiens CDNA clone  
IMAGE:3101688 5', mRNA sequence.  
CF143161  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
EST.  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 526)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4155 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
Tissue Procurement: Louis Staudt  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/humanfl.html>  
Seq primer: PYX-5  
Location/Qualifiers  
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FEATURES  
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/cell\_line="MGC85"  
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/clone\_lib="NIH MGC 52"  
/note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA  
(7.4-9.5kb). Directionally cloned. Cells provided by  
Louis M. Staudt, Ph.D. Library preparation by Maria de  
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "

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ORIGIN
Query Match      9.9%; Score 518.8; DB 14; Length 526;
Best Local Similarity 99.6%; Pred. No. 5.5e-80;
Matches 520; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1003 AGCCAGACAAATAATACCGGGTGTATTTGGGCTCAGACTCGACGTGCGACGTGGA 1062
DB 5 AGGCAGACAAATAATACCGGGTGTATTTGGGCTCAGACTCGACGTGCGACGTGGA 64

QY 1063 ACATTCCTGATTTCATCTCTCTATTTGTGATGTCCTCGGGTGTTCCTCACTAGAACCTTCAGAC 1122
DB 65 ACATTCCTGATTTCATCTCTCTATTTGTGATGTCCTCGGGTGTTCCTCACTAGAACCTTCAGAC 124

QY 1123 CCAATGTTATGAGAGAAAACCTTTAAAGAAATTTGAGGTGAGAGTTTGTTCAGAAATAT 1182
DB 125 CCAATGTTATGAGAGAAAACCTTTAAAGAAATTTGAGGTGAGAGTTTGTTCAGAAATAT 184

QY 1183 CACAGTAGCGTAGCTCAAGATCAAGCTCCATCTCGTAACACCATCCAGAGTTTGT 1242
DB 185 CACAGTAGCGTAGCTCAAGATCAAGCTCCATCTCGTAACACCATCCAGAGTTTGT 244

QY 1243 TCACGATGTCAAATTCATCATATGTCATCATCTAGTACTTCTAGCTTAGTTCAGAA 1302
DB 245 TCACGATGTCAAATTCATCATATGTCATCATCTAGTACTTCTAGTACTTAGTTCAGAA 304

QY 1303 AACAGCATAAAGATGAGAGGAGAGAGATGTCCTCTATTTGCTTGTGGCATGCTTGTAT 1362
DB 305 AACAGCATAAAGATGAGAGGAGAGATGTCCTCTATTTGCTTGTGGCATGCTTGTAT 364

QY 1363 GAAGAAGTCTTTACAGTGTGTGAGAGCGCTCGAGAACAAAGCTCCACCACTGCATG 1422
DB 365 GAAGAAGTCTTTACAGTGTGTGAGAGCGCTCGAGAACAAAGCTCCACCACTGCATG 424

QY 1423 TCATTTGGGAGAGAGGTGAGAGAAATAGAGAACCTTTAATATGTCCTGTTGTAGA 1482
DB 425 TCATTTGGGAGAGAGGTGAGAGAAATAGAGAACCTTTAATATGTCCTGTTGTAGA 484

QY 1483 TCTAAGTGGAGATCTCATGATTTCTACAGCCAGAGTTGTCA 1524
DB 485 TCTAAGTGGAGATCTCATGATTTCTACAGCCAGAGTTGTCA 526

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RESULT 12
CA512956      752 bp mRNA linear EST 15-NOV-2002
LOCUS        UI-R-FJ0-cqb-a-18-0-UI.r1 UI-R-FJ0 Rattus norvegicus cDNA clone
DEFINITION   UI-R-FJ0-cqb-a-18-0-UI 5', mRNA sequence.

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ACCESSION    CA512956
VERSION      CA512956.1 GI:25003910
KEYWORDS     EST.
SOURCE       Rattus norvegicus (Norway rat)
ORGANISM     Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

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REFERENCE    1 (bases 1 to 752)
AUTHORS     Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE       Normalization and subtraction: two approaches to facilitate gene
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
MEDLINE     97044477
PUBMED     8889548

```

```

COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565

```

Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
Seq primer: M13 REVERSE.

#### FEATURES

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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-R-FJ0"
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tissue(s): rat embryo. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pYX3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CATCTCTACT. This library
was created for the University of Iowa Program for Rat
Gene Discovery and Mapping (Val Sheffield, Bento Soares
and Tom Casavant)"

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#### ORIGIN

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Query Match      9.8%; Score 514; DB 14; Length 752;
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Matches 621; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

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ACCESSION BI656574.1 GI:15570810
VERSION    1
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL   1 (bases 1 to 719)
COMMENT   NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1835 Row: 0 Column: 06
High quality sequence stop: 719.
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            Library constructed by Life Technologies. Investigators
            Providing samples: Lothar Hennighausen/Priscilla Furth,
            NIH Reference for transgenic model: Li et al., Cell Growth
            and Differentiation 7, 3-11 (1996)."
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## ORIGIN

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Query Match      9.6%; Score 504; DB 12; Length 719;
Best Local Similarity 85.5%; Pred. No. 2.1e-77;
Matches 561; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
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CF287689
CF287689.1 GI:33647468
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Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 773)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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## RESULT 14

CF287689

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT





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; Publication No. US20040077044A1  
; GENERAL INFORMATION:  
; APPLICANT: YUE, Henry; DING, Li;  
; APPLICANT: LAL, Preeti G.; GRIFFIN, Jennifer A.;  
; APPLICANT: GURURAJAN Rajagopal; BAUGHN, Mariah R.;  
; APPLICANT: ISON, Craig H.; RAMKUMAR, Javalaxmi;  
; APPLICANT: TRIBOULEY, Catherine M.; SWARNAKAR, Anita;  
; APPLICANT: BURFORD, Neil; BANDMAN, Olga;  
; APPLICANT: THORNTON, Michael; KEAN, Farrah A.;  
; APPLICANT: WALIA, Narinder K.; NGUYEN, Damiel B.;  
; APPLICANT: ELLIOTT, Vicki S.; XU, Yuming;  
; APPLICANT: LU, Yan; HAFALIA, April J.A.;  
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;  
; APPLICANT: ARVIZU, Chandra S.; FORSYTHE, Ian J.  
; TITLE OF INVENTION: KINASES AND PHOSPHATASES  
; FILE REFERENCE: PI-0311 USN  
; CURRENT APPLICATION NUMBER: US/10/433.794  
; CURRENT FILING DATE: 2003-06-04  
; PRIOR APPLICATION NUMBER: PCT/US01/47431  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: US 60/254,034  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,814  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/255,756  
; PRIOR FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: US 60/256,172  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: US 60/257,416  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 60/260,912  
; PRIOR FILING DATE: 2001-01-10  
; PRIOR APPLICATION NUMBER: US 60/264,644  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: US 60/266,017  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PERL Program  
; SEQ ID NO 26  
; LENGTH: 4858  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: 7198931CBI  
US-10-433-794-26  
Query Match 90.5%; Score 4744.8; DB 17; Length 4858;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 4793; Conservative 0; Mismatches 22; Indels 5; Gaps 3;  
QY 7 ATGCGCGCGCGCGCGGGAATCGCGCTCTGCTGGGATTCGCGGCGCCAGGCTAG 66  
Db 1 ATGCGCGCGCGCGCGGGAATCGCGCTCTGCTGGGATTCGCGGCGCCAGGCTAG 60  
QY 67 AGCCCTGAGCGCGCGCGGAGCCCTCAAGCGAGAGCGCGCGCGCGCTGCC 126  
Db 61 AGCCCTGAGCGCGCGCGGAGCGGAGGCTCAAGCGAGAGCGCGCGCTGCC 120  
QY 127 GCGGGACTGCTGCGGAGCGGCGAGCGGGGCGCGGCGGCGAGCTGGCGGCGGG 186  
Db 121 GCGGGACTGCTGCGGAGCGGCGAGCGGGGCGCGGCGGCGAGCTGGCGGCGGG 180  
QY 187 CAGTGGCGAAAGTGGCGAGTGGAGCTGGACCTGCTGAGCAGCGGCTCTTCC 246  
Db 181 CAGTGGCGAAAGTGGCGAGTGGAGCTGGACCTGCTGAGCAGCGGCTCTTCC 240  
QY 247 GCGGCTTACCGCGGCGCTCTTCCGACTTCCCGAGAGCGCGGAGCGGCGGG 306  
Db 241 GCGGCTTACCGCGGCGCTCTTCCGACTTCCCGAGAGCGCGGAGCGGCGGG 300

QY 307 AGTGGGACCGGCTTCCAGCCTGTGGCGGTGGCGCGCGCCGCCACCGAGCGCGGCGCGC 366  
Db 301 AGTGGGACCGGCTTCCAGCCTGTGGCGGTGGCGCGCGCCGCCACCGAGCGCGGCGCGC 360  
QY 367 GGGCGCCACCTTACCGAGTGGTGGCGCGCGCGGACAGCGCGCGCTCGAGTCCCGCAGCG 426  
Db 361 GGGCGCCACCTTACCGAGTGGTGGCGCGCGCGGACAGCGCGCGCTCGAGTCCCGCAGCG 420  
QY 427 GCCGAGCCCGGGGAGAGCGCGCGCGCGCGCGCGCGCGCGCTCGTGGCAGCGCGCGCGCGC 486  
Db 421 GCCGAGCCCGGGGAGAGCGCGCGCGCGCGCGCGCGCGCGCTCGTGGCAGCGCGCGCGCGC 480  
QY 487 GGTCTGAGATGGAGAACTCTCAAGAGGTTGACAGAGTGGAGTATCGTCCA 546  
Db 481 GGTCTGAGATGGAGAACTCTCAAGAGGTTGACAGAGTGGAGTATCGTCCA 540  
QY 547 GAGGAAAGATGATCAGGGGAAACTGAGAGCAACCTGTATGCCAGCGCTGGAGGACGAA 606  
Db 541 GAGGAAAGATGATCAGGGGAAACTGAGAGCAACCTGTATGCCAGCGCTGGAGGACGAA 600  
QY 607 TGGTTGAAAGGAGAAATAGCGAGGCGCTGTGTGTGTAAGCAACCAATCCCAAGTTAAAGGA 666  
Db 601 TGGTTGAAAGGAGAAATAGCGAGGCGCTGTGTGTGTAAGCAACCAATCCCAAGTTAAAGGA 660  
QY 667 GATGGATCTGAAATGAATCACTTAGAGCTGAGTCTCCAGGAGGTTCCAGGCAAGTGGC 726  
Db 661 GATGGATCTGAAATGAATCACTTAGAGCTGAGTCTCCAGGAGGTTCCAGGCAAGTGGC 720  
QY 727 GCTTACACAGCTTCCAAAGGCGGACGAGCTCTTCTCTGCGCACTCCCATCAGGTGCG 786  
Db 721 GCTTACACAGCTTCCAAAGGCGGACGAGCTCTTCTCTGCGCACTCCCATCAGGTGCG 780  
QY 787 ACAGTGAATCAGAACTCCAGGAGTAAGGAGAAAGAGTTTCCCAAGTGCCTTTTCAG 846  
Db 781 ACAGTGAATCAGAACTCCAGGAGTAAGGAGAAAGAGTTTCCCAAGTGCCTTTTCAG 840  
QY 847 AGTGGCAGAAACACACACCGGAGAGCCCTTCCACAGATGCTTCTCACCATATAGC 906  
Db 841 AGTGGCAGAAACACACACCGGAGAGCCCTTCCACAGATGCTTCTCACCATATAGC 900  
QY 907 CCTGAGGAAACAAACCGCGGTGTTAAACAAAGTATGCGGGCCAGACTGTACTTACTGCG 966  
Db 901 CCTGAGGAAACAAACCGCGGTGTTAAACAAAGTATGCGGGCCAGACTGTACTTACTGCG 960  
QY 967 CAGATAGGCGCTTAAGTCTTCTGATGGAGAGACAGCCAGACATTAATACCGGGTG 1026  
Db 961 CAGATAGGCGCTTAAGTCTTCTGATGGAGAGACAGCCAGACATTAATACCGGGTG 1020  
QY 1027 TTTATTTGGCGCTCAGAACTGACGCTGTGACGTGGAACTTCTGTATTCATCTGCTATTT 1086  
Db 1021 TTTATTTGGCGCTCAGAACTGACGCTGTGACGTGGAACTTCTGTATTCATCTGCTATTT 1080  
QY 1087 GTGATGCTCGGGGTGTTTCACTAGAACCTTCCAGACCCCAATGTTATGGAGAAAACCTTTA 1146  
Db 1081 GTGATGCTCGGGGTGTTTCACTAGAACCTTCCAGACCCCAATGTTATGGAGAAAACCTTTA 1140  
QY 1147 AAGAAATTTGAGTTGAGAGTTTGTTCAGAAATATCACAGTAGCGTAGCTCAAGGATC 1206  
Db 1141 AAGAAATTTGAGTTGAGAGTTTGTTCAGAAATATCACAGTAGCGTAGCTCAAGGATC 1200  
QY 1207 AAGCTCCATCTGTPAACCACTCAGAAAGTTTGTTCACGATGTCAAAATCTCATACA 1266  
Db 1201 AAGCTCCATCTGTPAACCACTCAGAAAGTTTGTTCACGATGTCAAAATCTCATACA 1260  
QY 1267 TTGTCATCATCTAGTACTTCTACGTCTAGTTTCAGAAAACAGATAAAGGATGAGAGGAA 1326  
Db 1261 TTGTCATCATCTAGTACTTCTACGTCTAGTTTCAGAAAACAGATAAAGGATGAGAGGAA 1320  
QY 1327 CAGATGTGCTTATTTGCTTGTGGGCATGCTTGATGAGAAAGCTTTACAGTGTGTA 1386  
Db 1321 CAGATGTGCTTATTTGCTTGTGGGCATGCTTGATGAGAAAGCTTTACAGTGTGTA 1380

QY 1387 GACGGCTGCAGAAACAAGCTGCACACCACTGCATGTCAATTTGGGCGAAGAGTGTAGA 1446  
Db 1381 GACGGCTGCAGAAACAAGCTGCACCACTGCATGTCAATTTGGGCGAAGAGTGTAGA 1440  
QY 1447 AGAAATAGAGAAACCTTTAATATGTCCCTTTGTAGATCTAAGTGGAGATCTCATGATTTT 1506  
Db 1441 AGAAATAGAGAAACCTTTAATATGTCCCTTTGTAGATCTAAGTGGAGATCTCATGATTTT 1500  
QY 1507 TACAGCCAGAGTTGTCAAGTCCCTGTGTGATTTCCCTTCTCCCTCAGAGCTGCACAGCAG 1566  
Db 1501 TACAGCCAGAGTTGTCAAGTCCCTGTGTGATTTCCCTTCTCCCTCAGAGCTGCACAGCAG 1560  
QY 1567 CAAACCGTACAGCAGCAGCCTTTGGCTGGATCAAGAGGAATCAAGAGCAATTTTAAAC 1626  
Db 1561 CAAACCGTACAGCAGCAGCCTTTGGCTGGATCAAGAGGAATCAAGAGCAATTTTAAAC 1620  
QY 1627 CTTACTCATATTGGAACCTCAGCAAAATCCCTCTGTCTTACAAGATTTTACGTGAGCCATGG 1686  
Db 1621 CTTACTCATATTGGAACCTCAGCAAAATCCCTCTGTCTTACAAGATTTTACGTGAGCCATGG 1680  
QY 1687 ATTCAGGTGTTTGGAAATGGAACCTCGTTGGCTGCTTATTTCTAGAAAATGGAATGTGAGA 1746  
Db 1681 ATTCAGGTGTTTGGAAATGGAACCTCGTTGGCTGCTTATTTCTAGAAAATGGAATGTGAGA 1740  
QY 1747 GAGATGCGCCTCAGGCGTCTTTCCCATGATGTCAAGTGGGCGCTCTCTGCGCAATCGG 1806  
Db 1741 GAGATGCGCCTCAGGCGTCTTTCCCATGATGTCAAGTGGGCGCTCTCTGCGCAATCGG 1800  
QY 1807 GAGAGCACTGGAATAATTTCTGGGGGACAGAGTGAAGCAGCCCGAGTGGGGGAGCCACAGT 1866  
Db 1801 GAGAGCACTGGAATAATTTCTGGGGGACAGAGTGAAGCAGCCCGAGTGGGGGAGCCACAGT 1860  
QY 1867 GGGTCTTCCAGACCAAGTATCTCAGAGATGTGGTGGAGGATGTGCGAGCTTCTGICA 1926  
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QY 1927 ATGGTCTGTGCTGACCTGTCTACAAAGTGTACGTGTGCTTTTAAAAACATTTGAGAGCC 1986  
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QY 1987 ATGCTGGTATATACCTCTTGGCCACAGTTTGGCGGAAAGAAATCAAACTTCAGAGACTTCTC 2046  
Db 1981 ATGCTGGTATATACCTCTTGGCCACAGTTTGGCGGAAAGAAATCAAACTTCAGAGACTTCTC 2040  
QY 2047 CAGCCAGTTGTAGACACCACTCCTAGTCAAATGTGCAGATGCCAATAGCCGCAAGTCTAG 2106  
Db 2041 CAGCCAGTTGTAGACACCACTCCTAGTCAAATGTGCAGATGCCAATAGCCGCAAGTCTAG 2100  
QY 2107 CTGTCCATATCAACACTGTGTTGAACTGTGCAAGGCAAGGCAAGGAGTGGCAGTTGGC 2166  
Db 2101 CTGTCCATATCAACACTGTGTTGAACTGTGCAAGGCAAGGCAAGGAGTGGCAGTTGGC 2160  
QY 2167 AGAGAAATCTAAAGCTCGATCCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2226  
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QY 2227 ATTCTTTGGAACCAAACTCAATCAAACTCAAACTCAAACTCAAACTCAAACTCAAACTCA 2286  
Db 2221 ATTCTTTGGAACCAAACTCAATCAAACTCAAACTCAAACTCAAACTCAAACTCAAACTCA 2280  
QY 2287 ATAGATAGACTGTTGTTGGAATTTCCCTGCTGAAATTTTATCCCTCATATTTGTCAGTACTGAT 2346  
Db 2281 ATAGATAGACTGTTGTTGGAATTTCCCTGCTGAAATTTTATCCCTCATATTTGTCAGTACTGAT 2340  
QY 2347 GTTTCACAGCTGAGCCTGTTGAAATCAGGTATGAGAACTGTCTGCTCCCTCTTTAAACCTTT 2406  
Db 2341 GTTTCACAGCTGAGCCTGTTGAAATCAGGTATGAGAACTGTCTGCTCCCTCTTTAAACCTTT 2400  
QY 2407 GCTTTGAGTCCATTTGATTAATTTCCCACTCAATGGTTGGCAAACTTTCCAGAGAGTCTAC 2466  
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QY 2467 TTGAGTTCTGCAAGAATGGTTACTACAGTACCCCATGTGTGTTTCAAAAACATGTTTGAAGATG 2526











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; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No US20040404824A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: dt_Fl_genes Version 5.0
; SEQ ID NO 512
; LENGTH: 4696
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-112-944-512

Query March 87.1%; Score 4569; DB 13; Length 4696;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 4657; Conservative 0; Mismatches 30; Indels 10; Gaps 6;

QY 65 CGAGCCCTGAGGAGGCGGCGGAGAGCCCTCAAGGGAGCAGCGCGCGGCGTG 124
DB 2 CGAGCCCTGAGGAGGCGGCGGAGAGCCCTCAAGGGAGCAGCGCGGCGTG 61
QY 125 CCGGGGAGCTGCTCGGGAGGCGGCGGAGCGGGGGCGCGAGCGGGCGGAGCTGGCGGCGG 184
DB 62 CCGGGGAGCTGCTCGGGAGGCGGCGGAGCGGGGGCGCGAGCGGGCGGAGCTGGCGGCGG 121
QY 185 GGCAGCTGCGCAAGTCCGAGTGTGAGCTGAGCAGAGTGCCTGAGCAGCGCTCTTCC 244
DB 122 GGCAGCTGCGCAAGTCCGAGTGTGAGCTGAGCAGAGTGCCTGAGCAGCGCTCTTCC 181
QY 245 TTGCGGCTCACCGCGGCTCTCTCGACTTCCGCTCGCGGAGCGCGGAGCGGAGCGG 304
DB 182 TTGCGGCTCACCGCGGCTCTCTCGACTTCCGCTCGCGGAGCGCGGAGCGGAGCGG 241
QY 305 GGAGTGGAGCGGCTTCCAGCCTGTGCGGCTGCGGCGGCGGCGGCGGAGCGGAGCGG 364
DB 242 GGAGTGGAGCGGCTTCCAGCCTGTGCGGCTGCGGCGGCGGCGGAGCGGAGCGG 301
QY 365 CGCGCGCCACCTTACCGAGTCCGCTGCGGCGGCGGAGCGGCGGCTCGAGTCCCGCAG 424
DB 302 CGCGCGCCACCTTACCGAGTCCGCTGCGGCGGCGGAGCGGCGGCTCGAGTCCCGCAG 361
QY 425 CGCGCGGAGCGGCGGAGGAGCGGCGGCGGCGGCGGCGGCTCTCTGAGCGGCGGCGG 484
DB 362 CGCGCGGAGCGGCGGAGGAGCGGCGGCGGCGGCGGCGGCTCTCTGAGCGGCGGCGG 421
QY 485 CGGCTGTGAGATGGAGATTAAGAACTCTCAAGAGGTTGCAAGATGGATGATGCTC 544
DB 422 CGGCTGTGAGATGGAGATTAAGAACTCTCAAGAGGTTGCAAGATGGATGATGCTC 481
QY 545 CAGAGGAGCAATGATCAGGAGAGAACTGAAGGCAACTCTGATGCCAGCCTGGAAGCAG 604
DB 482 CAGAGGAGCAATGATCAGGAGAGAACTGAAGGCAACTCTGATGCCAGCCTGGAAGCAG 541
QY 605 AATGTTGGAAAGGAGAAATAGGCGAGGGCGCTGTGGTGGTAAACCAATCCAGTTAAG 664
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|                                                                         |     |                                                                |  |  |  |  |  |  |  |
|-------------------------------------------------------------------------|-----|----------------------------------------------------------------|--|--|--|--|--|--|--|
| ; APPLICANT: Bernards, Rene                                             |     |                                                                |  |  |  |  |  |  |  |
| ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients |     |                                                                |  |  |  |  |  |  |  |
| ; FILE REFERENCE: 9301-188-999                                          |     |                                                                |  |  |  |  |  |  |  |
| ; CURRENT APPLICATION NUMBER: US/10/342,887                             |     |                                                                |  |  |  |  |  |  |  |
| ; CURRENT FILING DATE: 2003-01-15                                       |     |                                                                |  |  |  |  |  |  |  |
| ; PRIOR APPLICATION NUMBER: 60/298,918                                  |     |                                                                |  |  |  |  |  |  |  |
| ; PRIOR FILING DATE: 2001-06-18                                         |     |                                                                |  |  |  |  |  |  |  |
| ; PRIOR APPLICATION NUMBER: 60/380,710                                  |     |                                                                |  |  |  |  |  |  |  |
| ; PRIOR FILING DATE: 2002-05-14                                         |     |                                                                |  |  |  |  |  |  |  |
| ; PRIOR APPLICATION NUMBER: 10/172,118                                  |     |                                                                |  |  |  |  |  |  |  |
| ; PRIOR FILING DATE: 2002-06-14                                         |     |                                                                |  |  |  |  |  |  |  |
| ; NUMBER OF SEQ ID NOS: 2699                                            |     |                                                                |  |  |  |  |  |  |  |
| ; SEQ ID NO 111                                                         |     |                                                                |  |  |  |  |  |  |  |
| ; LENGTH: 4693                                                          |     |                                                                |  |  |  |  |  |  |  |
| ; TYPE: DNA                                                             |     |                                                                |  |  |  |  |  |  |  |
| ; ORGANISM: Homo sapiens                                                |     |                                                                |  |  |  |  |  |  |  |
| US-1.0-342-887-111                                                      |     |                                                                |  |  |  |  |  |  |  |
| Query Match 87.0%; Score 4564.6; DB 13; Length 4693;                    |     |                                                                |  |  |  |  |  |  |  |
| Best Local Similarity 99.0%; Pred. No. 0;                               |     |                                                                |  |  |  |  |  |  |  |
| Matches 4647; Conservative 0; Mismatches 39; Indels 9; Gaps 5;          |     |                                                                |  |  |  |  |  |  |  |
| Qy                                                                      | 65  | CGAGCCCTGAGCGAGCGCGCGGAGAGCCCTCAAGCGAGCGAGCGCGCGCGGTG 124      |  |  |  |  |  |  |  |
| Db                                                                      | 2   | CGAGCCCTGAGCGAGCGCGCGGAGAGCCCTCAAGCGAGCGAGCGCGCGCGGTG 61       |  |  |  |  |  |  |  |
| Qy                                                                      | 125 | CGCGGGGACTGTCGCGGAGCGGCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCG 184      |  |  |  |  |  |  |  |
| Db                                                                      | 62  | CGCGGGGACTGCTGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 121      |  |  |  |  |  |  |  |
| Qy                                                                      | 185 | GGCAGCTGCGCAAGTGCGGAGTGTGAGTGTGACCAAGTGTCTGAGCAGCGCTTCTCC 244  |  |  |  |  |  |  |  |
| Db                                                                      | 122 | GGCAGCTGCGCAAGTGCGGAGTGTGAGCTGTGACCAAGTGTCTGAGCAGCGCTTCTCC 181 |  |  |  |  |  |  |  |
| Qy                                                                      | 245 | TTGCGCGCTCACCGCGGCTCTCGACTTTCCTCGCTGCGGAGCGCGGCGGCGGCGG 304    |  |  |  |  |  |  |  |
| Db                                                                      | 182 | TTGCGCGCTCACCGCGGCTCTCTCGACTTTCCTCGCTGCGGAGCGCGGCGGCGGCGG 241  |  |  |  |  |  |  |  |
| Qy                                                                      | 305 | GGAGTGGGACCGGCTTCAGCCTGTGCGGTGTCGCGCGCGCGCGCGCGCGCGCGCGCG 364  |  |  |  |  |  |  |  |
| Db                                                                      | 242 | GGAGTGGGACCGGCTTCAGCCTGTGCGGTGTCGCGCGCGCGCGCGCGCGCGCGCGCG 301  |  |  |  |  |  |  |  |
| Qy                                                                      | 365 | GGGGCGCCACCTTACCGAGTGGTGGCGGCGCGGAGACGCGCGCTCGAGTCCGCGAG 424   |  |  |  |  |  |  |  |
| Db                                                                      | 302 | GGGGCGCCACCTTACCGAGTGGTGGCGGCGCGGAGACGCGCGCTCGAGTCCGCGAG 361   |  |  |  |  |  |  |  |
| Qy                                                                      | 425 | CGGCCGAGCCCGGGGAGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 484  |  |  |  |  |  |  |  |
| Db                                                                      | 362 | CGGCCGAGCCCGGGGAGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 421  |  |  |  |  |  |  |  |
| Qy                                                                      | 485 | CCGGTCTGAGATGGAGAAATGAAGAACTCTCAAGAGGTTGCAAGATGGATGATCGTC 544  |  |  |  |  |  |  |  |
| Db                                                                      | 422 | CCGGTCTGAGATGGAGAAATGAAGAACTCTCAAGAGGTTGCAAGATGGATGATCGTC 481  |  |  |  |  |  |  |  |
| Qy                                                                      | 545 | CAGAGAAAGATGATCAGGAGAAACTGTGAGGCAACTGTATGCGCAGCTCGAGCAAGCG 604 |  |  |  |  |  |  |  |
| Db                                                                      | 482 | CAGAGAAAGATGATCAGGAGAAACTGTGAGGCAACTGTATGCGCAGCTCGAGCAAGCG 541 |  |  |  |  |  |  |  |
| Qy                                                                      | 605 | AATGTTGGAAGGAGAAATAGCGAGGCGCTGTGGTAAACCAATCCCAAGTAAAG 664      |  |  |  |  |  |  |  |
| Db                                                                      | 542 | AATGTTGGAAGGAGAAATAGCGAGGCGCTGTGGTAAACCAATCCCAAGTAAAG 601      |  |  |  |  |  |  |  |
| Qy                                                                      | 665 | GAGATGATCTGAATGAATCACTTAGCAGCTGAGTCTCCAGGAGAGGTCCAGCAAGTG 724  |  |  |  |  |  |  |  |
| Db                                                                      | 602 | GAGATGATCTGAATGAATCACTTAGCAGCTGAGTCTCCAGGAGAGGTCCAGCAAGTG 661  |  |  |  |  |  |  |  |
| Qy                                                                      | 725 | CGGCTTCACGAGCTTCCAAGCGCGACGCGAGTCTTCTCTGGCAATCCCCATCAGGTC 784  |  |  |  |  |  |  |  |
| Db                                                                      | 562 | CGGCTTCACGAGCTTCCAAGCGCGACGCGAGTCTTCTCTGGCAATCCCCATCAGGTC 721  |  |  |  |  |  |  |  |
| Qy                                                                      | 785 | GCACAGTGAATCAGAACTTCAGGAGTAAAGAGAAAGAGTGTCCCGAGTGCCTTTTC 844   |  |  |  |  |  |  |  |
| Db                                                                      | 722 | GCAAGTGAATCAGAACTTCAGGAGTAAAGAGAAAGAGTGTCCCGAGTGCCTTTTC 781    |  |  |  |  |  |  |  |

|    |     |                                                               |     |
|----|-----|---------------------------------------------------------------|-----|
| Qy | 665 | GAGATGATCTGAAATGAATCACTTTAGCAGCTGAGTCTTCAGAGAGAGGTTCAGGCAAGTG | 724 |
| Db | 602 | GAGATGATCTGAAATGAATCACTTTAGCAGCTGAGTCTTCAGAGAGAGGTTCAGGCAAGTG | 661 |
| Qy | 725 | CGGTTTCACAGGTTCCAAAGGCCGACGAGTCTTTCTCTGGCAAATCCCCCAATCAGGTC   | 784 |
| Db | 662 | CGGTTTCACAGGTTCCAAAGGCCGACGAGTCTTTCTCTGGCAAATCCCCCAATCAGGTC   | 721 |
| Qy | 785 | GCACAGTGAATCAGAAATCTCCAGAGTAAAGGAGNAAAAGATTTCGCCAGTGCCCTTTC   | 844 |
| Db | 722 | GCA CAGTGAATCAGAAATCTCCAGAGTAAAGGAGNAAAAGATTTCGCCAGTGCCCTTTC  | 781 |











QY 2165 GCAGAGAAATCTAAAAGCTGGATCCATTTGGTATTTGGTGTGTGATTAATGCTTAAAT 2224  
DB 2102 GCAGAGAAATCTAAAAGCTGGATCCATTTGGTATTTGGTGTGTGATTAATGCTTAAAT 2161  
QY 2225 GTATTTCTGGAAAACCAAACTGAAATCAAACTTGGCAAGAACTTCTGGCCGCTTTGTC 2284  
DB 2162 GTATTTCTGGAAAACCAAACTGAAATCAAACTTGGCAAGAACTTCTGGCCGCTTTGTC 2221  
QY 2285 TTATAGATAGACTGTTGTTGGAATTTCTGCTGAAATTTATCTCATTTGTCAGTACTG 2344  
DB 2222 TTATAGATAGACTGTTGTTGGAATTTCTGCTGAAATTTATCTCATTTGTCAGTACTG 2281  
QY 2345 ATGTTTCAAGAGCTGAGCTGTTGAAATCAGGTATAGAGAGCTGCTGCTCTTAACT 2404  
DB 2282 ATGTTTCAAGAGCTGAGCTGTTGAAATCAGGTATAGAGAGCTGCTGCTCTTAACT 2341  
QY 2405 TTGCTTTGAGCTGCTGATTAATTTCCCACTCAATGTTGCAAACTTCCAGAGAGTCT 2464  
DB 2342 TTGCTTTGAGCTGCTGATTAATTTCCCACTCAATGTTGCAAACTTCCAGAGAGTCT 2401  
QY 2465 ACTTGAGTTCTGCAAGAAATGTTACTACAGTACCCCATGTTTCAAACTGTTAGAAA 2524  
DB 2402 ACTTGAGTTCTGCAAGAAATGTTACTACAGTACCCCATGTTTCAAACTGTTAGAAA 2461  
QY 2525 TGCTGAGTTTCCAG---TTCCACTCACTTCCAGAGTGGCTGCGCTTTGATGGCTA 2581  
DB 2462 TGCTGAGTTTCCAGTGTTCAGTGTTCCTTCCAGAGTGGCTGCGCTTTGATGGCTT 2521  
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DB 2522 ATGAGATGAGTGGAAATTTCCGAGCCATCCAGTTGGCGTAGAGACACTTTACAAC 2581  
QY 2642 GTCAACAGGACAGC--TTCTTGTGAGGATCTGTTCCCAACAATCTCTGGAACCAACA 2699  
DB 2582 GACAAACAACAACAGCTTTTGAGGAGTCTGTTCCCAACAATCTCTGGAACCAACA 2641  
QY 2700 GAACAGTTTCCCC--TGAGTGCACTGTCATTTAGAGAAAATGGAAGGATTAATGCTA 2758  
DB 2642 GAACAGTTTCCCCCTTGAGTGCACTGTCATTTAGAGAAAATGGAAGGATTAATGCTA 2701  
QY 2759 CAATAATGAGTGCCAGTTTCAGAGACATTTCTGAGACCTGGCCAGCATTTAGTAGGAC 2818  
DB 2702 CAATAATGAGTGCCAGTTTCAGAGACATTTCTGAGACCTGGCCAGCATTTAGTAGGAC 2761  
QY 2819 CTTCTAGTTCAACAACAACAACAACAACAAGAGCAACCAAGCCCAATGGTTCAAA 2878  
DB 2762 CTTCTAGTTCAACAACAACAACAACAACAAGAGCAACCAAGCCCAATGGTTCAAA 2821  
QY 2879 CAAAAGGAGAGCCCAAGTCAGTGTGTTGAATCTCTCTCTTTATCTCATCTTCCCAAT 2938  
DB 2822 CAAAAGGAGAGCCCAAGTCAGTGTGTTGAATCTCTCTCTTTATCTCATCTTCCCAAT 2881  
QY 2939 TAATGTTTCCAGCTTTGCAACCCCTTCTTCTTACCCCATCTGTAACAGCTGGCACTG 2998  
DB 2882 TAATGTTTCCAGCTTTGCAACCCCTTCTTCTTACCCCATCTGTAACAGCTGGCACTG 2941  
QY 2999 CAACAGATGTTCTTAAGCATAGACTTCAGGGATTCATTTCCCTGAGAAATACCTTCTGCAT 3058  
DB 2942 CAACAGATGTTCTTAAGCATAGACTTCAGGGATTCATTTCCCTGAGAAATACCTTCTGCAT 3001  
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## RESULT 7

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US-10-152-319A-2042
; Sequence 2042, Application US/10152319A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castile, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/10/152,319A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2042
; LENGTH: 5180
; TYPE: DNA
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; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_053887
US-10-152-319A-2042
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Matches 4020; Conservative 0; Mismatches 647; Indels 91; Gaps 12;

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 3643 GGAGAGATATCATCATTTATTCAAGATACACAGAGACTCTACCAGGACATACCAAA 3702  
 QY |||||  
 3594 GGAGAGATATTTATCATTTCTCAGCAGGACACACCAAGAACTCTTCCAGGACATACCAAA 3653  
 Db |||||  
 3703 GCAAAACAAACCGTATAGAGAGACACTGAATGGCTGAAAGGTCACACAGATAGGCCCTTGA 3762  
 QY |||||  
 3654 GCAAAACAGCTTTACAGAGAGAGCTGAGTGGCTGAAAGGCCAGCAGATAGGCCCTCGA 3713  
 Db |||||  
 3763 GCATTTCTTTCTTTATCAGGCTCAAGATGTGGAACTTGBAACTTTAATGGCTGTAAA 3822  
 QY |||||  
 3714 GCATTTCTTTCTTTATCCTTACCAAGCACAGGATGTGGGACTTGGGACTTTAATGGCTGTAAA 3773  
 Db |||||  
 3823 CAGTGCACTTATCTCAGAAACACATCTTCTGACAAAGAAAGTGTAGTAAGCACATAGA 3882  
 QY |||||  
 3774 CAGTGCACTTATCTCAGAAACACATCTTCTCAGAGAGAGGAGTGTGGAGAGCTTGAGG 3833  
 Db |||||  
 3883 GAAGAGATAAGATGATGAGCCATCTGAATCAATCAATCAATCAATCAATCAATCAATCA 3942  
 QY |||||  
 3834 GAAGAGATCCGATGATGGTCACTCAACCATCAATCAATCAATCAATCAATCAATCAATCA 3893  
 Db |||||  
 3943 ACCTGTGAGAGAGCAATTTACATCTCTTCTTCAATGAAATGGAATGGAGGGGATCGGTGGCT 4002  
 QY |||||  
 3894 ACCTGTGAGAGAGCAATTTACATCTCTTCTTCAATGAAATGGAATGGAGGGGATCGGTGGCT 3953  
 Db |||||  
 4003 CATTTGCTGATGATGAGGCTTTCAAGAAATCAGTGTATTAATCACTACATGAAACAG 4062  
 QY |||||  
 3954 CACCTCTTGTAGTAAATACGGAGCTTTCAAGAGTCACTGCTCATTAACACTACACTGAGCAG 4013  
 Db |||||  
 4063 TTACTCGTGGCTTTCTGATCTCCATGAACCAATCAATCAATCAATCAATCAATCAATCA 4122  
 QY |||||  
 4014 TTACTCGTGGCTTTCTGATCTCTTCCAGGAAACAGATCAATTCACAGAGACGTCAGAGGT 4073  
 Db |||||  
 4123 GCCAATTTGCTAATTTGACAGCACTGTGTCAGAGACTTAAGAAATTCAGATTTTGGAGCTGCA 4182  
 QY |||||  
 4074 GCCAATTTGCTAATTTGACAGCACTGTGTCAGAGACTTAAGAAATTCAGATTTTGGAGCTGCT 4133  
 Db |||||  
 4183 GCCAGTTGGCATCAAAAGGAACTGTGTGAGAGAGTTTCAAGGACAAATTTACTTGGGACAC 4242  
 QY |||||  
 4134 GCCAGTTGGCATCAAAAGGAACTGTGTGAGAGAGTTTCAAGGACAAATTTACTTGGGACAC 4193  
 Db |||||  
 4243 ATTCATTTATGCACTGTGAGTACTAAGAGGTCACAGTGTGAAAGGAGCTGTGATGTA 4302  
 QY |||||  
 4194 ATTCATTTATGCACTGTGAGTACTAAGAGGTCACAGTGTGAAAGGAGCTGTGATGTA 4253  
 Db |||||  
 4303 TGGAGTGTGCTGTGATTTATAGAAATGCTTGTGCAAAACCCACCATGGAATTCAGAA 4362  
 QY |||||  
 4254 TGGAGTGTGCTGTGATTTATAGAAATGCTTGTGCAAAACCCACCATGGAATTCAGAA 4313  
 Db |||||  
 4363 AAAACACTCCATCATCTTGTCTTGTATTTAAGATTTGTAGTGCACACTTACTGTCCATTCG 4422  
 QY |||||  
 4314 AAAACACTCCATCATCTTGTCTTGTATTTAAGATTTGTAGTGCACACTTACTGTCCATTCG 4373  
 Db |||||  
 4423 ATCCCTTCACATTTGTCTCTGTTTACAGATGTGGCTCTTGTGTTTGAATCACTTCA 4482  
 QY |||||

|    |      |                                                                 |      |
|----|------|-----------------------------------------------------------------|------|
| Db | 4374 | ATCCGTCACACCTGTGCCCGGGTCTGCCGACGTGGCGCGTGGCTGTAGAACTTCAG        | 4433 |
| Qy | 4483 | CCTCAGGACAGACCTCCATCAAGAGAGCTACTGAGCATCCAGTCTTTCGTACTACATGG     | 4542 |
| Db | 4434 | CCTCAGGACCGGCTCGTCCAGNGAGCTGCTGAAACATCCGGTCTCCGTACCACTGG        | 4493 |
| Qy | 4543 | TAGCCAAATTGCGAGATCAACTACAGTAGAAACGAGATGCTCAACAGAGAGAAAAAACT     | 4602 |
| Db | 4494 | TAGTTAAATTGTTTCAGATCAGTCTTAATGGAGACAGGATATGCAACCGGAGAGAGAAAG    | 4553 |
| Qy | 4603 | TG----TGGGGAAACCATTTGATATCTACTGGCCATGATGCCACTGCAACGACTATGAAC    | 4658 |
| Db | 4554 | AGAACTTGTGGGCGACCATCGCGTAAACCGGAGCCCTACGCGCACTGAACGACGAGAAC     | 4613 |
| Qy | 4659 | GAGGCGAGTGGGGAAACCCCTTACCTAAGTATGTGAATTGCAAAATCATGATCTGTACCTAAG | 4718 |
| Db | 4614 | GGGGCCACGCGGGAA--CGTACCTAAGCATGTGATTTGCAAAATCATGACCTGTACCTAAG   | 4672 |
| Qy | 4719 | CTCAGTATGCA--AAGGCCCAAACTAGTGCAGAAACTGTAAACTGTGCGCTTTCAGAGAACT  | 4777 |
| Db | 4673 | CTCGATATGCAGACATCTACAGTCTCGTCAGGAACTGCACACCGTGCCTTTTCACAGACT    | 4732 |
| Qy | 4778 | GGCCCTTAGGTCAAACAGGAAAAAATGAAGTTTTCATGACTAAATTGCAGAGAGCATATTT   | 4837 |
| Db | 4733 | GSCCTCGGGGACACAGAGAGCGGATGGAGTTTTCATGACTAAAGAACAGAGCATTAATT     | 4792 |
| Qy | 4838 | TATTTTTTTGAGCAGCTTTTTCAGCAA                                     | 4864 |
| Db | 4793 | TA--TTTTTGGAGCAGCTTTTTCAGTA                                     | 4817 |

## RESULT 9

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US-10-000-864-7
; Sequence 7, Application US/10000864
; Publication No. US20020146798A1
; GENERAL INFORMATION:
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES
; FILE REFERENCE: CFI-085C2PC
; CURRENT APPLICATION NUMBER: US/10/000,864
; CURRENT FILING DATE: 2001-10-31
; EARLIER APPLICATION NUMBER: 09/423,890
; EARLIER FILING DATE: 2000-06-03
; EARLIER APPLICATION NUMBER: PCT/US99/05556
; EARLIER FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: US98 60/078,153
; EARLIER FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: US98 60/099,165
; EARLIER FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 5253
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(4493)
US-10-000-864-7

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Query Match      65.1%; Score 3417; DB 14; Length 5253;
Best Local Similarity 83.5%; Pred. No. 0;
Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;

QY 1 GAGAAATGGCGGCGGCGGCGGGAATCGCGCTCTGTCTGGGATTCGCGGCGCGCAGG 60
Db 9 GAGAAATGGCGGCGGCGGCGGCGATCGCGCTCTGTCTGGGATTCGCGGCGCGCG 68

QY 61 GTACGAGCCCTCAGGCAGCGCGCGG-----GGAGAGCCCTCAAGCGCAGCAGC 111
Db 69 GCGGCGAGTCCCGAGGCGGCGCGCGCGGCGGAGGAGAGAGAGTCTCCAGGAAGCGCG 128

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|      |    |                                                                 |
|------|----|-----------------------------------------------------------------|
| 112  | QY | CGCCCC--GCGGTCGCCGGGACGTCTGCGGAGGCGGCGAGCGGGGCCGCGAGCGG168      |
| 123  | Db | CGCCCCCGACGCGGCGCGGCGGGCTGCTGCGGAGACCTGCGCAGCGCGGCGCGAGCGC188   |
| 169  | QY | CGGACTGGCGGCGGCGGAGCTGCGCAAGTGCAGTGTGGAGCTGGACACAGCTGCCT228     |
| 189  | Db | CGGACTGGCGGCGGCGGCGAGTGCAGAGTGTGGAGCTGGACACAGCTGCGC248          |
| 229  | QY | GAGCAGCGCTCTTCTTTCGCGCTCACCGCGGCT--CCTCGACTTCCCGCTCGCGC285      |
| 249  | Db | GAGCAGCGCTCTTCTTTCGCGCGGCTCGCGCGCTGCCCATCTACTTCCCGCTCGCGC308    |
| 286  | QY | GAGCCCGCGACGACGCGGCGAGTGGGACCGGCTTCCAGCCTGTGGCGGTGCGCGCGCCC345  |
| 309  | Db | GAGCCCGCGACCGGCTCAGAGCGAGTCTTCAGCCCGCGCGGAGCGCGACCC368          |
| 346  | QY | CACGAGCGCGAGCGCGCGCGCGCCACTTACCGAGTCGTTGCGCGCGCGCGCGACG405      |
| 369  | Db | CGGAGCGCGAGTGCCTCGCGCTCCCACTCTGCCGAGCTGGCGCGCGCGCGGAGC428       |
| 406  | QY | GCGCGCTCGAGTCCCGCAGCGCGCGAGCGCGGAGAGCGGCGCGCGCGCGCGAGCGG465     |
| 429  | Db | GCGCGCGGAGCCCGCGGG-----GCGGAGCGG458                             |
| 466  | QY | TCTCTCAGCGGCCCCCGGTCGTGAGATGGAGATTAAGAACTCTCAAGGGTTG525         |
| 489  | Db | CCCTCTGAGCGGCCCCCTCGGTGAGAGATGGAGATAAAGAAACCTCAAGAGACTG518      |
| 526  | QY | CACAAGATGGATGATCGTCAGAGGAACGAATGATCAGGAGAACTGAAGGCAACCTGT585    |
| 549  | Db | CACAAGATGGAGATCGCCCGGAGGAGAAATGATCCGGAGAGCTCAAGGCGACCTGT578     |
| 586  | QY | ATGCCACCTGGAGACGACGATGTTTGGAAAGGAGAAATAGCGAGGCGCTGTGGTGA645     |
| 579  | Db | ATGCCGCTGGAGACGACGATGTTTGGAGAGGAGAAACAGAGAGGCGCTGTGGTGG638      |
| 646  | QY | AAACCAATCCAGTTAAAGGAGTGGATCTGAATCGAATCACTTAGCAGCTGAGTCTCCA705   |
| 639  | Db | AAGCAATCCCTATTAAGAGATGGATCTGAATGAATACTTGGCAGCTGAGCCCCAG698      |
| 706  | QY | GGAGAGTCCAGGCAAGTCGGCTTCCACAGCTTCCGAAGCGCGAGCGAGCTCTTCTCCT765   |
| 639  | Db | GGAGAGGCCAGGAGGTTCCGCTGCACGAGCCCAAGGCCGACAGGCCCATCTCCT758       |
| 766  | QY | GGCAACTCCCCATCAGTGCACAGTGAATCAGAACTCCAGGAGTAAGGAGAAAAAGA825     |
| 759  | Db | GCGAGCTCTCGTCAGGCGCTCGGTGAAGCGGGAATCCCGAGGAGTAAGACGGAACGA818    |
| 826  | QY | GTTTCCCCAGTGCCTTTCAGAGTGCAGATCACACACCCCGAAGAGCCCTTCCACA885      |
| 819  | Db | GTGTCCCGGTGCTTTCAGAGTGCAGATCACACACCCCGAAGAGCCCCATCACCG878       |
| 886  | QY | GATGCTTTCACCATATAGCTGAGGAAACAAACCGCGTGTAAACAAAGTATGCGG945       |
| 879  | Db | GATGCTTCTCCCGTACAGCCGACAGGAGAGCAGCGCGCGGTGAACAAAGTATGAGA938     |
| 946  | QY | GCCAGCTGTACTTACTGCAGCAGATAGGCGCTAATCTTCTCTGATTGGAGGAGACAGC1005  |
| 939  | Db | CCAGAGCTGTACTCTGCAGCAGATAGAACCCAACTCTTCTCTGATTGGAGGAGACAGT958   |
| 1006 | QY | CCAGACAATAAATACCGGGTGTATTGGGCTCAGAACTGCAGCTGTCACGTTGGAACA1065   |
| 999  | Db | CCAGACAATAAATACCGGGTGTATTGGGCGCACAGAACTGCAGCTGTGGCGCTGGAGCA1058 |
| 1066 | QY | TTCGTATTCACTGTCTATTGTGATGCTCGGGGTGTTTCAACTAGAACCTTCAGACCCA1125  |
| 1059 | Db | TTCGTATTCACTCTTGTGTGATGCTCGGGTGTTCAGCTAGAACCTCTGACCCC1118       |
| 1126 | QY | ATGTTATGGAGAAAACTTTAAGAAATTGAGGTTGAGATTTGTTCAGGAATATCAC1185     |
| 1119 | Db | ATGTTATGGAGAAAACTTTAAAAAATTTCCGAGTTGAGAGTTGTTCAGGAATATCAC1178   |
| 1186 | QY | AGTAGGCGTAGCTCAAGGATCAAGCTCCATCTCGTAAACCACTCCAGAGCTTGTGTCA1245  |

1179 AGTAGCGTAGCTCAGAAATCAAGCTCCATCCGGACACCATCCAGAGTTTGTGCA 1238  
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1239 CGCATGTCAAAATCTCAACATATGTCTATCATCTAGTACTTCTAGTCTAGTTCAGAAAC 1298  
1306 AGCATAAAGAGTGAAGAGGACAGATGTCTATTTCTGTTGGGCATCTTGTATGAA 1365  
1299 AGCATCAAGATGAAGAGGACGATGTCTCCATCTGCTGGGCATCTGATGAG 1358  
1366 GAAAGCTTACAGTGTGTGAAGACGGCTGCAAGAAACAGCTGACACCATCTGATGCA 1425  
1359 GAGAGCTGACTGTGTGAAGATGGCTGCAAGAAACAGCTGACACCATCTGATGTC 1418  
1426 ATTTGGGACAGAGAGTGTGAAGAAATAGAGAACTTTAATATGTCCTCTTTGTAGATCT 1485  
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1539 TCCCTCGAGCTGTCCAGAGCCATCTCTCCCGCAGCAGCCGCTGGCCGATCACAGCG 1598  
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1663 TACAAAGATTTAGCTGAGCCATGATTTAGTGTGTTGAATGGAATCTGTTGGCTGCTTA 1722  
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1719 TTTCTAGAACTGGAAATGTGAGAGATGGCCCTTAGCGCTCTTTCCCATGATGTCAGT 1778  
1783 GGGGCCCTGCTGTGCAATGGGAGACACTGGAAATCTGGGGCAGCAGTGGAGC 1842  
1779 GGGGCCCTGCTGTGTCNAACGGGAGAGACACTGGAAATCTGGAGGCGGAGTGGGGC 1838  
1843 AGCCGAGTGGGGGAGCCACAGTGGGTCTTCCAGACCAAGTATCTCAGGAGATGTGGTG 1902  
1839 AGCTTAAAGCGGGAGGGCCAGCGGTCTCCAGCCAGCATCTCAGGGATGTGGTG 1898  
1903 GAGGCGATGTGACGCTTGTGCAATGGCTGTGCTGACCTGTCTACAAAGTGTACGTT 1962  
1899 GAGGCGGTGTGCAATGTCTGTCTATAGTGTGCGCTGACCCCTGTCTACAAAGTGTACGTT 1958  
1963 GCTGCTTTAAACATTTGAGAGCCATGCTGATATATCTCTTGGCCACAGTTTAGCGGAA 2022  
1959 GCTGCTTTAAACATTTGAGAGCCATGCTGATATACCTCTTGGCCACAGTCTGGCAGAA 2018  
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2019 AGAATCAAACTTCAAGACCTTCCAGCCAGTGTGTAGACACTATCTGTCTCAAGTGTGA 2078  
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2079 GATGCCAATAGCCGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2138  
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2199 GGTGTTGATGCTTTAAATTTGATTTCTGGAAACCAACTGAAATCAAAATTTGGCAA 2258  
2263 GAACTTCTTGGCCGCTTTGTCTTATAGATGATGTTGTTGGAATTTCTCTGTAATTT 2322

2259 GAACTGCTGGCTGGCTGTCTTATAGACAGGTTGTGTTGGAAATTTCTCTGCTGAATTC 2318  
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2383 AGCTGCTGCTCTCTTAACCTTTGCTTTGAGTCCATGATTAATTTCCACATCAATGTTT 2442  
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2832 AAGCCAGCGGTTCAAAACAAAGGACAGACCCACAGTCAAGTGTGTAATCTCTCTCTTTG 2891  
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2892 TC---TCTCATTAATTAATGTTTCCAGCAGCTCAGCCCTTGTCTCTCTCTCTCTCTCTCT 2948  
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3283 GACAGCTTTGGCTGAGCAGAAATAGTATGTTGTTATCCAGTGTGACAGACAGT 3342  
3234 GACAGCTTTGGCGGGCGGCAACAGTGGCAACCGCTCATACCCAGGAGGAGACAGT 3293  
3343 TTCACCCAGTGTAGAGGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3402  
3294 TTCACCCGCTGGAGGACAAAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 3353



Db 121 AGTCCAGGCAAGTGGCGCTTACCAGCTTCCAAAGCCGACGAGTCCCTTCTCTGGCA 180  
QY 770 ACTCCCATCAGTTCGACAGTGAATCAGAACTCTCAGAGTAAAGAGAAAGAGTTT 829  
Db 181 ACTCCCATCAGTTCGACAGTGAATCAGAACTCTCAGAGTAAAGAGAAAGAGTTT 240  
QY 830 CCCAGTGCCTTTTCAGAGTGGAGATCAGACACACCCCGAAGAGCCCTTCCACAGATG 889  
Db 241 CCCAGTGCCTTTTCAGAGTGGAGATCAGACACACCCCGAAGAGCCCTTCCACAGATG 300  
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QY 950 GACTGTACTTACTCAGCAGATAGGCGCTAACTCTTCTCTGANTGGAGGAGACAGCCAG 1009  
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QY 1130 TATGGAGAAACCTTAAAGATTTTGAAGTTTGAGTTTGAGTTTCTCCAGAAATATCACAGTA 1189  
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QY 1190 GCGGTAGTCAAGGATCAAGCTCCATCTCGTAAACACCATCCAGAAAGTTTGTTCACGCA 1249  
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QY 1250 TGTCAAAATTCATACATGTCATCTAGTACTTCTACGTCTAGTTTCAGAAACAGCA 1309  
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QY 2390 TGTCCCTTCTTAACTTTGTTTGGCTCAGTCCATTAATTAATTTCCCACTCAATGTTGGCAAAAC 2449  
Db 1801 TGTCCCTTCTTAACTTTGTTTGGCTCAGTCCATTAATTAATTTCCCACTCGATGTTGGCAAGC 1860  
QY 2450 TTTCCAGAGGATCTACTTTGAGTTCTGCAAGATGTTTACTACAGTACCCCATGTGTGTTT 2509  
Db 1861 TCTCTCGAGAGATATATCTGAGCTCTGCCAGATGTTGAGCCGAGTGCCTGTGTGTTT 1920  
QY 2510 CAAAACTGTTTGAAGATGCTGAGTGTTCAGTGTTCACCTCACTTCAACAGATGCGTGCCT 2569  
Db 1921 CCAAGCTGGTAAACCATGCTTAATGCTTCTGGCTCCACCCACTTCAACAGATGCGGCGGC 1980  
QY 2570 GTTTGATGGCTATTTGAGATGAGGTGGAATTTGCCGAAGCCATCCAGTTGGGCGTAGAAG 2629  
Db 1981 GTCTGATGGCTATTCGGGATGAGGTAGAAATTTCCGAGGTCTATCCAGCTGGGTGTGGAGG 2040  
QY 2630 ACATTTTGAATGTTCAACAGGACAGCTTCTTTCAGGCACTCTGTTCACCAACACTATCTGG 2689  
Db 2041 ACATTTTGAATGTTCAACAGGACAGCTTCTTTCAGGCACTCTGTTCACCAACACTATCTGG 2095  
QY 2690 AAACCCAGAGAACAGTTTCCCTGAGTGCACAGTCCATTTAGAGAAACTGGAAGAGAT 2749  
Db 2096 -----AGAAAACAGTCCCTTTGACACACAGTCCATATAGAGAAACTTGAAGAGGAC 2148  
QY 2750 TATGTGCTCAAAAATTTGAGTGCAGTTTCAAGAGACATTTTCTGAGAGACTGGCCAGCATTTT 2809  
Db 2149 TATGTGCTACAGACTGAGTGCAGTCCGAGGACATTTCTGACAGACTGGCCGGGTCT 2208  
QY 2810 CAGTAGAACCTTCTAGTTTCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2869  
Db 2209 CTGTAGACTTCCAGCT-----CAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2953  
QY 2870 TGGTTCAAAACAAAGGAGAGCCCAAGTCAAGTGTGTTGAATCTCTCTCTCTTTATCTCATC 2929  
Db 2254 CGGTTCAAAACAAAGGAGAGCCCAAGTCAAGTGTGTTGAATCTCTCTCTCTTTGCT---TC 2310









|      |    |                                                                    |      |
|------|----|--------------------------------------------------------------------|------|
| 966  | DB | TAACTGTGCGCTTCAAAGAACTGGGCCCTAGGTGAACAGGAAACAATGAAGTTTGTGATG       | 1025 |
| 4815 | QY | ACTAAATTGCAGAAGCATAATTTATTTTTTGGAGCACATTTTTTCAGCAATATTAGCGGC       | 4874 |
| 1026 | DB | ACTAAATTGCAGAAGCATAATTTATTTTTTGGAGCACATTTTTTCAGCAATATTAGCGGC       | 1085 |
| 4875 | QY | TGAGGGGCTCAGACATCTATTTTTTAATATTTCAAAATATTTCTTCCATTTTCATATAGTGATCAC | 4934 |
| 1086 | DB | TGAGGGGCTCAGACATCTATTTTTTAATATTTCAAAATATTTCTTCCATTTTCATATAGTGATCAC | 1145 |
| 4935 | QY | AAGCAGGGGGTCTCGCAATTTCCGTTCAAATTTTTTGTGCATCGGCTATAAAATCGATATCT     | 4994 |
| 1146 | DB | AAGCAGGGGGTCTCGCAATTTCCGTTCAAATTTTTTGTGCATCGGCTATAAAATCAGATATCT    | 1205 |
| 4995 | QY | GCCTCTTTTAGGTCAGAGTATGCTATCAGTAGCAATACATACATATATTTTTTAAAGTTG       | 5054 |
| 1206 | DB | GCCTCTTTTAGGTCAGAGTATGCTATCAGTAGCAATACATACATATATTTTTTAAAGTTG       | 1265 |
| 5055 | QY | ATACTCTTTATGACCCACAGTTGACCTTTATTTTTCTTAAATACCAGGCAGTTGTGGCT        | 5114 |
| 1266 | DB | ATACTCTTTATGACCCACAGTTGACCTTTATTTTTCTTAAATACCAGGCAGTTGTGGCT        | 1325 |
| 5115 | QY | CATTGTGCATTTTACTGTGTGGCCCATTCATTTCGTTTTTGGAAATTATGGTTTGTATTT       | 5174 |
| 1326 | DB | CATTGTGCATTTTACTGTGTGGCCCATTCATTTCGTTTTTGGAAATTATGGTTTGTATTT       | 1385 |
| 5175 | QY | TCATGTTTATTTACATTCATTTTTTTGTATTTACAGGGAAGCTGATCTTTTTTTTCAAAACC     | 5234 |
| 1386 | DB | TCATGTTTATTTACATTCATTTTTTTGTATTTACAGGGAAGCTGATCTTTTTTTTCAAAACC     | 1445 |
| 5235 | QY | AAAAAAAAAA 5244                                                    |      |
| 1446 | DB | AAAAAAAAAA 1455                                                    |      |

RESULT 13

US-09-796-692-6957/c  
Sequence 6957, Application US/09796692  
Publication No. US20020198362A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Algate, Paul A.  
APPLICANT: Mannion, Jane  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF  
HEMATOLOGICAL MALIGNANCIES  
FILE REFERENCE: 2077.001200  
CURRENT APPLICATION NUMBER: US/09/796.692  
CURRENT FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: 60/186,126  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/222,903  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: 60/223,416  
PRIOR FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: 60/223,378  
PRIOR FILING DATE: 2000-08-07

```

; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: PatSEQ for Windows Version 3.0
; SEQ ID NO 6957
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (528)
; OTHER INFORMATION: n=A,T,C or G
US-09-796-692-6957

Query Match      10.5%; Score 549; DB 9; Length 550;
Best Local Similarity 99.8%; Pred. No. 1.9e-138;
Matches 549; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2251 AACAAATTGGCAAGAACTCTTGGCCGCCCTTGTCTTATAGATAGACTGTGTGTGGAAATTT 2310
DB 550 AACAAATTGGCAAGAACTCTTGTGNCGCCCTTGTCTTATAGATAGACTGTGTGTGGAAATTT 491

QY 2311 CTTGCTGAATTTATCTCTATATGTTCAGTACTGATGTTTCAAGCTGAGCCTGTGGAA 2370
DB 490 CTTGCTGAATTTATCTCTATATGTTCAGTACTGATGTTTCAAGCTGAGCCTGTGGAA 431

QY 2371 ATCAGGTATAGAAGCTGTGCTCCCTCTTAAACCTTTGCTTTGCAGTCCCATTTGATAATTC 2430
DB 430 ATCAGGTATAGAAGCTGTGCTCCCTCTTAAACCTTTGCTTTGCAGTCCCATTTGATAATTC 371

QY 2431 CACTCAATGTTGGCAAACTTTTCAGNAGGATCTACTTGAGTTTCTCAAGAATGGTTACT 2490
DB 370 CACTCAATGTTGGCAAACTTTTCAGNAGGATCTACTTGAGTTTCTCAAGAATGGTTACT 311

QY 2491 ACAGTACCCCATGTGTTTTCAAAACCTGTTAGAAAATGCTGAGTGTTCCTCAGTCCACTCAC 2550
DB 310 ACAGTACCCCATGTGTTTTCAAAACCTGTTAGAAAATGCTGAGTGTTCCTCAGTCCACTCAC 251

QY 2551 TTCCACAGGATCGTGCCTCTTTGATGGCTATTGCGAGATCAGGTGGGAAATTCGCGAAGCC 2610
DB 250 TTCCACAGGATCGTGCCTCTTTGATGGCTATTGCGAGATCAGGTGGGAAATTCGCGAAGCC 191

QY 2611 ATCCAGTTGGCGGTAGAAGACACTTTTGGATGGTCAACAGGACAGCTTCTTCAGGCACT 2670
DB 190 ATCCAGTTGGCGGTAGAAGACACTTTTGGATGGTCAACAGGACAGCTTCTTCAGGCACT 131

QY 2671 GTTCCCAACACTATCTGGAACCCACAGAGACAGTTCCCTCAGTGCACAGTCCATTTA 2730
DB 130 GTTCCCAACACTATCTGGAACCCACAGAGACAGTTCCCTCAGTGCACAGTCCATTTA 71

QY 2731 GAGAAAACTGGAAAGGATTATGTGCTACAAAATTTAGTCCAGTTCAGAGGACATTTCT 2790
DB 70 GAGAAACTGGAAAGGATTATGTGCTACAAAATTTAGTGCAGTTCAGAGGACATTTCT 11

QY 2791 GAGAGACTGG 2800
DB 10 GAGAGACTGG 1

RESULT 14
US-10-040-862-6957/c
; Sequence 6957, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126

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PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: US 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: US 60/223,416  
PRIOR FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: US 60/223,378  
PRIOR FILING DATE: 2000-08-07  
PRIOR APPLICATION NUMBER: US 08/796,692  
PRIOR FILING DATE: 2001-03-01  
NUMBER OF SEQ ID NOS: 10467  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6957  
LENGTH: 550  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (528)  
OTHER INFORMATION: n=A,T,C or G  
US-10-040-862-6957

Query Match 10.5%; Score 549; DB 15; Length 550;  
Best Local Similarity 99.8%; Pred. No. 1.9e-138;  
Matches 549; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2251 AACAAATGGCAAGAACTTCTTGGCGCTTTGCTTATAGATAGACTGTTGGAAATTT 2310  
Db 550 AACAAATGGCAAGAACTTCTTGGCGCTTTGCTTATAGATAGACTGTTGGAAATTT 491  
Qy 2311 CTGCTGAAATTTATCTCTCATATTTGTCAGTACTGTTTACAGAGCTGAGCTGTTGAA 2370  
Db 490 CTGCTGAAATTTATCTCTCATATTTGTCAGTACTGTTTACAGAGCTGAGCTGTTGAA 431  
Qy 2371 ATCAGGTATAAGAGCTGCTGCTCTCTTAACCTTTGCTTTCAGTCCATTGATAATTC 2430  
Db 430 ATCAGGTATAAGAGCTGCTGCTCTCTTAACCTTTGCTTTCAGTCCATTGATAATTC 371  
Qy 2431 CACTCAATGGTTGGCAAACTTTCAGAGGATCTACTGATTTCTGCAAGATGTTACT 2490  
Db 370 CACTCAATGGTTGGCAAACTTTCAGAGGATCTACTGATTTCTGCAAGATGTTACT 311  
Qy 2491 ACAGTACCCCATGCTGTTTCAAACTGTAGAAATGCTGAGTGTTCAGTTCACCTCAC 2550  
Db 310 ACAGTACCCCATGCTGTTTCAAACTGTAGAAATGCTGAGTGTTCAGTTCACCTCAC 251  
Qy 2551 TTCACAGAGATCGTGGCGCTTTGATGCTATTCAGATAGGTGGAAATTCGAGGCC 2610  
Db 250 TTCACAGAGATCGTGGCGCTTTGATGCTATTCAGATAGGTGGAAATTCGAGGCC 191  
Qy 2611 ATCCAGTTGGGCGTAGAGACACTTTGGATGTTCAACAGGACAGCTTCTTCAGGCACT 2670  
Db 190 ATCCAGTTGGGCGTAGAGACACTTTGGATGTTCAACAGGACAGCTTCTTCAGGCACT 131  
Qy 2671 GTTCCCAACAACTATCTGAAACCCAGAGAACAGTTCCTCCCTGAGTGCACAGTCAATTA 2730  
Db 130 GTTCCCAACAACTATCTGAAACCCAGAGAACAGTTCCTCCCTGAGTGCACAGTCAATTA 71

Qy 2731 GAGAAACTGAAAGAGATATGCTACAAAATTGAGTGCCAGTTCCAGAGCAATTTCT 2790  
Db 70 GAGAAACTGAAAGAGATATGCTACAAAATTGAGTGCCAGTTCCAGAGCAATTTCT 11  
Qy 2791 GAGAGACTGG 2800  
Db 10 GAGAGACTGG 1

RESULT 15

US-10-057-475B-6957/C  
Sequence 6957, Application US/10057475B  
Publication No. US20040002068A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Algate, Paul A.  
APPLICANT: Mannion, Jane  
APPLICANT: Clapper, Jonathan David  
APPLICANT: Wang, Aijun  
APPLICANT: Ordenez, Nadia  
APPLICANT: Carter, Lauren  
APPLICANT: McNeill, Patricia Dianne  
APPLICANT: Corixa Corporation  
TITLE OF INVENTION: Hematological Malignancies  
FILE REFERENCE: 014058-014402US  
CURRENT APPLICATION NUMBER: US/10/057,475B  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: US 60/186,126  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: US 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 10979  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6957  
LENGTH: 550  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(550)  
OTHER INFORMATION: n = g, a, c or t  
US-10-057-475B-6957

Query Match 10.5%; Score 549; DB 16; Length 550;  
Best Local Similarity 99.8%; Pred. No. 1.9e-138;  
Matches 549; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2251 AACAAATGGCAAGAACTTCTTGGCGCTTTGCTTATAGATAGACTGTTGGAAATTT 2310  
Db 550 AACAAATGGCAAGAACTTCTTGGCGCTTTGCTTATAGATAGACTGTTGGAAATTT 491  
Qy 2311 CTGCTGAAATTTATCTCTCATATTTGTCAGTACTGTTTCAAGCTGAGCTGTTGAA 2370  
Db 490 CTGCTGAAATTTATCTCTCATATTTGTCAGTACTGTTTCAAGCTGAGCTGTTGAA 431

|    |      |                                                                 |      |
|----|------|-----------------------------------------------------------------|------|
| Qy | 2371 | ATCAGGTATAGAAGCTGCTGCTCCCTCTTAAACCTTTGCTTTGCGAGTCCCAITGATAATTCC | 2430 |
| Db | 430  | ATCAGGTATAGAAGCTGCTGCTCCCTCTTAAACCTTTGCTTTGCGAGTCCCAITGATAATTCC | 371  |
| Qy | 2431 | CACTCATGGTTGCGAAACCTTTCCAGAAAGGATCTACTTTGAGTTCTCGAAGATGGTTACT   | 2490 |
| Db | 370  | CATCTAATGGTTGCGAAACCTTTCCAGAAAGGATCTACTTTGAGTTCTCGAAGATGGTTACT  | 311  |
| Qy | 2491 | ACAGTACCCCATGTGTTTCAAACCTGTTAGAAATGCTGAGTGTTCAGATTCCACTCAC      | 2550 |
| Db | 310  | ACAGTACCCCATGTGTTTCAAACCTGTTAGAAATGCTGAGTGTTCAGATTCCACTCAC      | 251  |
| Qy | 2551 | TTCAACAGGATCGTGCCCGTTTGATGGCTATTGCAGATGAGGTGGAAATTGCCGAAGCC     | 2610 |
| Db | 250  | TTCAACAGGATCGTGCCCGTTTGATGGCTATTGCAGATGAGGTGGAAATTGCCGAAGCC     | 191  |
| Qy | 2611 | ATCCAGTTGGCGCTAGAAGACACTTTTGGATGGTCAACAGGACAGCTTCTTGCAGGCACT    | 2670 |
| Db | 190  | ATCCAGTTGGCGCTAGAAGACACTTTTGGATGGTCAACAGGACAGCTTCTTGCAGGCACT    | 131  |
| Qy | 2671 | GTTCCTCAACAACATCTGGAAACCAACAGAGAACAGTTCCCTCCTGAGTGCAAGTCCATTTA  | 2730 |
| Db | 130  | GTTCCTCAACAACATCTGGAAACCAACAGAGAACAGTTCCCTCCTGAGTGCAAGTCCATTTA  | 71   |
| Qy | 2731 | GAGAAAACTGGAAAAGGATTATGTGCTACAAAATTGAGTGCAGTTCAGAGGACATTTCT     | 2790 |
| Db | 70   | GAGAAAACCTGGAAAAGGATTATGTGCTACAAAATTGAGTGCAGTTCAGAGGACATTTCT    | 11   |
| Qy | 2791 | GAGAGACTGG                                                      | 2800 |
| Db | 10   | GAGAGACTGG                                                      | 1    |









|    |      |                      |                                                |      |
|----|------|----------------------|------------------------------------------------|------|
| QY | 4261 | GAGGTACTAGAGGTC      | CAACAGTATGGAAGGAGCTGTGATGTATGAGTGTGGCTGTGCT    | 4320 |
| DB | 4261 | GAGGTACTAGAGGTC      | CAACAGTATGGAAGGAGCTGTGATGTATGAGTGTGGCTGTGCT    | 4320 |
| QY | 4321 | ATTATAGAAATGCTTGTG   | CAAAACCAACCATGGAATGCAGAAAAACACTCCAAATCATCTT    | 4380 |
| DB | 4321 | ATTATAGAAATGCTTGTG   | CAAAACCAACCATGGAATGCAGAAAAACACTCCAAATCATCTT    | 4380 |
| QY | 4381 | GCCTTGATATTTAAGAT    | TGCTAGTGGAACTACTGTGCTCCATCGATCCCTTCACATTGTCT   | 4440 |
| DB | 4381 | GCCTTGATATTTAAGAT    | TGCTAGTGGAACTACTGTGCTCCATCGATCCCTTCACATTGTCT   | 4440 |
| QY | 4441 | CCCTGGTTTACGAGAT     | TGCGCTCTTCGTTGTTTAAAGAACTTCAACCTCAGACAGACCTCCA | 4500 |
| DB | 4441 | CCCTGGTTTACGAGAT     | TGCGCTCTTCGTTGTTTAAAGAACTTCAACCTCAGACAGACCTCCA | 4500 |
| QY | 4501 | TCAGAGAGCTACTGAAGCA  | TCCAGTCTTCGTTACTACATGGTGTAGCCAAATATGCGATC      | 4560 |
| DB | 4501 | TCAGAGAGCTACTGAAGCA  | TCCAGTCTTCGTTACTACATGGTGTAGCCAAATATGCGATC      | 4560 |
| QY | 4561 | AACTACAGTAGAAACAGAGT | GCTCAAACAGAGAAAAAAACCTTGTGGGAAACCAATTGA        | 4620 |
| DB | 4561 | AACTACAGTAGAAACAGAGT | GCTCAAACAGAGAAAAAAACCTTGTGGGAAACCAATTGA        | 4620 |
| QY | 4621 | TATTTCTACTGCGCAATG   | CCACTGACAGCTATGACAGGCGCAGTGGGGAACCCCTTAC       | 4680 |
| DB | 4621 | TATTTCTACTGCGCAATG   | CCACTGACAGCTATGACAGGCGCAGTGGGGAACCCCTTAC       | 4680 |
| QY | 4681 | CTAAGTATGTGATTTGACA  | AAATCATGTCTGTACCTAAGCTCAGTATGCAAAAGCCCAAAAC    | 4740 |
| DB | 4681 | CTAAGTATGTGATTTGACA  | AAATCATGTCTGTACCTAAGCTCAGTATGCAAAAGCCCAAAAC    | 4740 |
| QY | 4741 | TAGTGCAGAAACCTGTAA   | CTGTCCTTTCAAAGAACTGGCCCTAGGTGGAACAGGAAAAACA    | 4800 |
| DB | 4741 | TAGTGCAGAAACCTGTAA   | CTGTCCTTTCAAAGAACTGGCCCTAGGTGGAACAGGAAAAACA    | 4800 |
| QY | 4801 | ATGAAGTTTGCATGACTAA  | ATTTGAGAGCAATAATTTATTTTTTGGAGCACTTTTCA         | 4860 |
| DB | 4801 | ATGAAGTTTGCATGACTAA  | ATTTGAGAGCAATAATTTATTTTTTGGAGCACTTTTCA         | 4860 |
| QY | 4861 | GCAATATTTAGCGGCTGAG  | GGGCTCAGGATCTATTTTAATATTTCAATTTCTTCCTCATTT     | 4920 |
| DB | 4861 | GCAATATTTAGCGGCTGAG  | GGGCTCAGGATCTATTTTAATATTTCAATTTCTTCCTCATTT     | 4920 |
| QY | 4921 | CATATAGTATGATCAACAG  | CAGGGGTTCTGCAATTCGGTCAAAATTTTTTGTCACTGGCTA     | 4980 |
| DB | 4921 | CATATAGTATGATCAACAG  | CAGGGGTTCTGCAATTCGGTCAAAATTTTTTGTCACTGGCTA     | 4980 |
| QY | 4981 | TAAATACAGTATCTGCC    | CTTTTAGGTCAGAGTATGCTATGAGTAGCAATACATACATAT     | 5040 |
| DB | 4981 | TAAATACAGTATCTGCC    | CTTTTAGGTCAGAGTATGCTATGAGTAGCAATACATACATAT     | 5040 |
| QY | 5041 | ATTTTAAAGTTGATCTCT   | TTATGACCCACAGTTGACCTTTATTTCTTAATACCA           | 5100 |
| DB | 5041 | ATTTTAAAGTTGATCTCT   | TTATGACCCACAGTTGACCTTTATTTCTTAATACCA           | 5100 |
| QY | 5101 | GGGCAGTTGTGGCTCAT    | TGTGCAATTTACTGTGGCCCAATCATTTCTTTTGGAAATT       | 5160 |
| DB | 5101 | GGGCAGTTGTGGCTCAT    | TGTGCAATTTACTGTGGCCCAATCATTTCTTTTGGAAATT       | 5160 |
| QY | 5161 | ATGGTTTGTATTTTTCAT   | GTATTTATTCATTTTGTATTTCAGGGAAGCTGATC            | 5220 |
| DB | 5161 | ATGGTTTGTATTTTTCAT   | GTATTTATTCATTTTGTATTTCAGGGAAGCTGATC            | 5220 |
| QY | 5221 | TTTTTTTTTCAAACCA     | AAAAA 5245                                     |      |
| DB | 5221 | TTTTTTTTTCAAACCA     | AAAAA 5245                                     |      |

|          |          |         |     |        |                 |
|----------|----------|---------|-----|--------|-----------------|
| RESULT 2 |          |         |     |        |                 |
| AX780290 |          |         |     |        |                 |
| LOCUS    | AX780290 | 5238 bp | DNA | linear | PAT 14-JUL-2003 |

Sequence 2447 from Patent WO030239443.  
 AX780290 AX780290.1 GI:32697284

Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Haerlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S.,  
 Dugas, M., Ellis, R., Brors, B., and Mergenthaler, S.  
 Novel genetic markers for leukemias  
 Patent: WO 030239443-A 2447 15-MAY-2003;  
 Deutsches Krebsforschungszentrum (DK);  
 Ludwig-Maximilians-Universität München (DE);  
 PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)

FEATURES  
 Location/Qualifiers  
 1..5238  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN  
 Query Match 96.2%; Score 5043.6; DB 6; Length 5238;  
 Best Local Similarity 98.3%; Pred. No. 0;  
 Matches 5102; Conservative 0; Mismatches 79; Indels 8; Gaps 3

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| QY | 65  | CGAGCCCTGAGCAGCGCGCGCGAGGAGCCCTCAAGGCGAGCAGCGCGCGCGGCTG      | 124 |
| DB | 2   | CGAGCCCTGAGCAGCGCGCGCGAGGAGCCCTCAAGGCGAGCAGCGCGCGGCTG        | 61  |
| QY | 125 | CCGCGGGACTCTCTCGGAGCGCGGCGAGCGGGGCGCGAGCGGCGACTTGGCGCGCG     | 184 |
| DB | 62  | CCGCGGGACTCTCTCGGAGCGCGGCGAGCGGGGCGCGAGCGGCGACTTGGCGCGCG     | 121 |
| QY | 195 | GGAGCTCGCAAGTGGGAGTGTGGAGCTGGACCACTGCCCTGAGCAGCGCTCTTCC      | 244 |
| DB | 122 | GGAGCTCGCAAGTGGGAGTGTGGAGCTGGACCACTGCCCTGAGCAGCGCTCTTCC      | 181 |
| QY | 245 | TTGCGGCTTCAACCGCGGCTCTCTGACTTCCCGCTCGCGAGCGCGCGGACGCGG       | 304 |
| DB | 182 | TTGCGGCTTCAACCGCGGCTCTCTGACTTCCCGCTCGCGAGCGCGCGGACGCGG       | 241 |
| QY | 305 | GGAGTGGACCGGCTTCAGACTGTGGCGGTGCGCGCGCCCAACGAGCGCGGCGCG       | 364 |
| DB | 242 | GGAGTGGACCGGCTTCAGACTGTGGCGGTGCGCGCGCCCAACGAGCGCGGCGCG       | 301 |
| QY | 365 | GGCGGCGCCACTTACCGAGTCGGTGGCGGCGCGGACAGCGCGCTCGAGTCCGCGAG     | 424 |
| DB | 302 | GGCGGCGCCACTTACCGAGTCGGTGGCGGCGCGGACAGCGCGCTCGAGTCCGCGAG     | 361 |
| QY | 425 | CGCGCGAGCCGGGAGAAAGCGGCGCGCGCGCGAGCGCTCTCTCGAGCGGCGCGCG      | 484 |
| DB | 362 | CGCGCGAGCCGGGAGAAAGCGGCGCGCGCGCGAGCGCTCTCTCGAGCGGCGCGCG      | 421 |
| QY | 485 | CCGGTCTGTGAGATGAGAAATAAGAAATCTCTCAAAGGGTTGCACAGATGGATGTC     | 544 |
| DB | 422 | CCGGTCTGTGAGATGAGAAATAAGAAATCTCTCAAAGGGTTGCACAGATGGATGTC     | 481 |
| QY | 545 | CAGAGAACGAATGATCAGGAGAAACTGAAGCGAACCTGTATGCCAGCTCGAAGCAGC    | 604 |
| DB | 482 | CAGAGAACGAATGATCAGGAGAAACTGAAGCGAACCTGTATGCCAGCTCGAAGCAGC    | 541 |
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Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Yue, H., Ding, L., Lal, P.G., Griffin, J.A., Gururajan, R.,  
Baughin, M.R., Ison, C.H., Ramkumar, J., Tribouley, C.M., Swarnakar, A.,  
Burford, N., Bandman, O., Thornton, M., Khan, F.A., Wallia, N.K.,  
Nguyen, D.B., Elliott, V.S., Xu, Y., Lu, Y., Hafalia, A.J., Yos, M.G.,  
Gandhi, A.R., Arvizu, C. and Porsythe, I.  
Kinases and phosphatases  
TITLE Kinases and phosphatases  
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INCYTE Genomics, Inc. (US)  
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|    |      |                                                                 |      |
|----|------|-----------------------------------------------------------------|------|
| QY | 1505 | TCTACAGCCACGAGTTGTCAAGTCTGTGGATTCCCTTCTTCCCTCAGAGCTGCACAGC      | 1564 |
| DB | 1442 | TCTACAGCCACGAGTTGTCAAGTCTGTGGATTCCCTTCTTCCCTCAGAGCTGCACAGC      | 1501 |
| QY | 1565 | AGCAACCGCTACAGCAGCAGCTTTGGCTGGATCAGGAGGAAATCAAGAGCAATTTT        | 1624 |
| DB | 1502 | AGCAACCGCTACAGCAGCAGCTTTGGCTGGATCAGGAGGAAATCAAGAGCAATTTT        | 1561 |
| QY | 1625 | ACCTTACTCATTATGAACTCAGCAAAATCCCTCCTGCTTACAAAGATTAGCTGAGCCAT     | 1684 |
| DB | 1562 | ACCTTACTCATTATGAACTCAGCAAAATCCCTCCTGCTTACAAAGATTAGCTGAGCCAT     | 1621 |
| QY | 1685 | GGATTCCAGCTGTTGGAATGGAACTCGTTGGCTGCTTATTTCTAGAAACTGGAATGCA      | 1744 |
| DB | 1622 | GGATTCCAGCTGTTGGAATGGAACTCGTTGGCTGCTTATTTCTAGAAACTGGAATGCA      | 1681 |
| QY | 1745 | GAGAGATGGCCCTCAGCGCTTTTCCCATGATGTAGTGGGGCCCTGCTGTGTGGCAATG      | 1804 |
| DB | 1682 | GAGAGATGGCCCTCAGCGCTTTTCCCATGATGTAGTGGGGCCCTGCTGTGTGGCAATG      | 1741 |
| QY | 1805 | GGGAGAGCACTGGAAATCTGGGGGCGAGCAGTGGAAAGCAGCCGAGTGGGGAGCCACA      | 1864 |
| DB | 1742 | GGGAGAGCACTGGAAATCTGGGGGCGAGCAGTGGAAAGCAGCCGAGTGGGGAGCCACA      | 1801 |
| QY | 1865 | GTGGGTCTTCCCAGACCACTATCTCAGGAGATGTGTGGAGGCAATGCTGCGCGTTCTGT     | 1924 |
| DB | 1802 | GTGGGTCTTCCCAGACCACTATCTCAGGAGATGTGTGGAGGCAATGCTGCGCGTTCTGT     | 1861 |
| QY | 1925 | CAATGCTCTGTGCTGACCCCTGCTCACAAGAGTGACGTTGCTGCTTTTAAAAACATTGAGAG  | 1984 |
| DB | 1862 | CAATGCTCTGTGCTGACCCCTGCTCACAAGAGTGACGTTGCTGCTTTTAAAAACATTGAGAG  | 1921 |
| QY | 1985 | CCATGCTGTATATPACTCTTGGCCACAGTTTAGCGGAAAGAAATCAAACCTTCAGAGACTTC  | 2044 |
| DB | 1922 | CCATGCTGTATATPACTCTTGGCCACAGTTTAGCGGAAAGAAATCAAACCTTCAGAGACTTC  | 1981 |
| QY | 2045 | TCGAGCCAGTGTAGACACCATCTAGTCAAAATGTCAGATGCCAATAGCCGACACAAGTC     | 2104 |
| DB | 1982 | TCGAGCCAGTGTAGACACCATCTAGTCAAAATGTCAGATGCCAATAGCCGACACAAGTC     | 2041 |
| QY | 2105 | AGCTGTCCATATCAACACTGTTGMACTGTGCAAAAGCCAAAGCAGGAGGTTGGCAGTTG     | 2164 |
| DB | 2042 | AGCTGTCCATATCAACACTGTTGMACTGTGCAAAAGCCAAAGCAGGAGGTTGGCAGTTG     | 2101 |
| QY | 2165 | GCAGAGAAATACAAAAGCTGGATCCATTGGTATTTGGTGGTGTGATTATGTCTTAAATT     | 2224 |
| DB | 2102 | GCAGAGAAATACAAAAGCTGGATCCATTGGTATTTGGTGGTGTGATTATGTCTTAAATT     | 2161 |
| QY | 2225 | GTATTTCTGGAAAACCAAACTGAATCAAACAATTTGGCAAGAACTTCTTGGCGCCTTTGTC   | 2284 |
| DB | 2162 | GTATTTCTGGAAAACCAAACTGAATCAAACAATTTGGCAAGAACTTCTTGGCGCCTTTGTC   | 2221 |
| QY | 2285 | TTATAGATAGACTGTTGTTGGAAATTTCCCTGCTGAAATTTTATCTCATATTTGTCAGTACTG | 2344 |
| DB | 2222 | TTATAGATAGACTGTTGTTGGAAATTTCCCTGCTGAAATTTTATCTCATATTTGTCAGTACTG | 2281 |
| QY | 2345 | ATGTTTCCAAAGCTGAGCCCTGTTGAAATCAGGTATTAAGAAGCTGCTGCTCCTCTTAACCT  | 2404 |
| DB | 2282 | ATGTTTCCAAAGCTGAGCCCTGTTGAAATCAGGTATTAAGAAGCTGCTGCTCCTCTTAACCT  | 2341 |
| QY | 2405 | TTGCTTTGCAGTCAATTGATTAATTTCCCACTCAATGGTTGGCAAACTTCCAGAGGATCT    | 2464 |
| DB | 2342 | TTGCTTTGCAGTCAATTGATTAATTTCCCACTCAATGGTTGGCAAACTTCCAGAGGATCT    | 2401 |
| QY | 2465 | ACTTGAGTCTTCGAAGATGGTTACTACAGTACCCTCATGTGTTTCAAACTGTTAGAAA      | 2524 |
| DB | 2402 | ACTTGAGTCTTCGAAGATGGTTACTACAGTACCCTCATGTGTTTCAAACTGTTAGAAA      | 2461 |
| QY | 2525 | TGCTGAGTGTTCGAG---TTCCACTCACTTCAACAGGATGCGTGGCGTTGATGCTA        | 2581 |
| DB | 2462 | TGCTGAGTGTTCGAGTGTTCCTCACTCACTTCAACAGGATGCGTGGCGTTGATGCTT       | 2521 |

|    |      |                                                                 |      |
|----|------|-----------------------------------------------------------------|------|
| Qy | 2582 | TTGCAGATGAGTGGGAATTTGCCAGAGCCATCCAGTTGGCGTAGAAGACACTTTTCGATG    | 2641 |
| Db | 2522 | ATGCAGATGAGTGGGAATTTGCCAGAGCCATCCAGTTGGCGTAGAAGACACTTTTCGATG    | 2581 |
| Qy | 2642 | GTCACACGACAGC--TTCTTGACGACATCTGTTCCCAACAACATATCTGGAACCCACAGA    | 2699 |
| Db | 2562 | GACAAACAACAACAGCTTTTGCAGGCATCTGTTCCCAACAACATATCTGGAACCCACAGA    | 2641 |
| Qy | 2700 | GAACAGTTCCCC--TGAGTGCACAGTCCATTTAGAGAAACCTCGAAAGGATTTATGTCTA    | 2758 |
| Db | 2642 | GAACAGTTCCCTTTGAGTGCACAGTCCATTTAGAGAAACCTCGAAAGGATTTATGTCTA     | 2701 |
| Qy | 2759 | CAAAATTTGAGTGCAGTTTCAGAGGACAATTTCTGAGAGACTGGCCAGGATTTTCAGTAGGAC | 2818 |
| Db | 2702 | CAAAATTTGAGTGCAGTTTCAGAGGACAATTTCTGAGAGACTGGCCAGGATTTTCAGTAGGAC | 2761 |
| Qy | 2819 | CTTCTAGTTTCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA    | 2878 |
| Db | 2762 | CTTCTAGTTTCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA    | 2821 |
| Qy | 2879 | CAAAAGGACAGCCCCACAGTCAGTGTGAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT     | 2938 |
| Db | 2822 | CAAAAGGACAGCCCCACAGTCAGTGTGAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT     | 2881 |
| Qy | 2939 | TAATGTTTTCAGACCTCTGCAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT     | 2998 |
| Db | 2882 | TAATGTTTTCAGACCTCTGCAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT     | 2941 |
| Qy | 2999 | CAAACAGATGCTCTAAGCATAGACTTCAGGGATTCATTCCTGACAGAAATACCTTCCTGAT   | 3058 |
| Db | 2942 | CAAACAGATGCTCTAAGCATAGACTTCAGGGATTCATTCCTGACAGAAATACCTTCCTGAT   | 3001 |
| Qy | 3059 | CTCCTCAAAACAACAGCGCAAGTTTTCTCTCAAAATTCACAGAAAATGTCCTGAAACAAAG   | 3118 |
| Db | 3002 | CTCCTCAAAACAACAGCGCAAGTTTTCTCTCAAAATTCACAGAAAATGTCCTGAAACAAAG   | 3061 |
| Qy | 3119 | ACTCAGATAAATCTTCCAGTCTTTTACTCAGTCAAGACCTTCCCTCCAGTAACATAC       | 3178 |
| Db | 3062 | ACTCAGATAAATCTTCCAGTCTTTTACTCAGTCAAGACCTTCCCTCCAGTAACATAC       | 3121 |
| Qy | 3179 | ACAGGCCAAAGCCACTAGACCTACCCACAGGTAAACAAGTAAACAGGGAGATCCCTCAA     | 3238 |
| Db | 3122 | ACAGGCCAAAGCCACTAGACCTACCCACAGGTAAACAAGTAAACAGGGAGATCCCTCAA     | 3181 |
| Qy | 3239 | AAATAGCATACACTTGATGCTGAACAGTAGTTCCTCAATGTGATGACAGCTTTGCGTGA     | 3298 |
| Db | 3182 | AAATAGCATACACTTGATGCTGAACAGTAGTTCCTCAATGTGATGACAGCTTTGCGTGA     | 3241 |
| Qy | 3299 | GCAGCAATAGTAGTAATGCTGTTATACCCAGTGCAGACAGTGTTCACCCAGTAGAGG       | 3358 |
| Db | 3242 | GCAGCAATAGTAGTAATGCTGTTATACCCAGTGCAGACAGTGTTCACCCAGTAGAGG       | 3301 |
| Qy | 3359 | AGAAATGACAGATTAGATGCTCAATACAGAGCTCACTCCAGTATTTGAGAGACCTTCTTGAG  | 3418 |
| Db | 3302 | AGAAATGACAGATTAGATGCTCAATACAGAGCTCACTCCAGTATTTGAGAGACCTTCTTGAG  | 3361 |
| Qy | 3419 | CATCTATGCCCTTCAGTGATACAACAGTAACCTTTTAAAGTCAGAGTGTCTGCTCTGCTC    | 3478 |
| Db | 3362 | CATCTATGCCCTTCAGTGATACAACAGTAACCTTTTAAAGTCAGAGTGTCTGCTCTGCTC    | 3421 |
| Qy | 3479 | CTGAAAGGCTGAAATGATGATACCTTCAAGATGATGTCGAATCAATCAAAAGTCA         | 3538 |
| Db | 3422 | CTGAAAGGCTGAAATGATGATACCTTCAAGATGATGTCGAATCAATCAAAAGTCA         | 3481 |
| Qy | 3539 | AAGAGAAGATGGAAGCTGAAAGAAGAAGCTTTTAGCAATTTGCCATGCAATGTCAGCGT     | 3598 |
| Db | 3482 | AAGAGAAGATGGAAGCTGAAAGAAGAAGCTTTTAGCAATTTGCCATGCAATGTCAGCGT     | 3541 |
| Qy | 3599 | CTCAGGATGCCCTCCCATAGTTTCTCCTCAGCTGCAGGTTGAAATGAGAGATATCATCA     | 3658 |
| Db | 3542 | CTCAGGATGCCCTCCCATAGTTTCTCCTCAGCTGCAGGTTGAAATGAGAGATATCATCA     | 3601 |
| Qy | 3659 | TTATTCAACAGGATACACACAGACACTCTACACAGGACATACCAAGACAAACCAACCGTATA  | 3718 |





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Db 69 GCGCGAGTCCCGAGGCGCGCGCGGCGGAGGAGGAGCTCTCCAGGGAAGCGGC 128  
QY 112 GCGGCC---GCGGCTGCGCGGAGCTGCTGCGGAGGCGGCGGAGCGCGCGGAGCGG 168  
Db 129 GCGCGCGAGCGGCGGCGGCGGCTGCTGCGGAGCGCTGGCAGCGCGGCGCGGAGCGC 188  
QY 169 GCGGACTGCGGCGGCGGAGCTGCGCAAGTGGGAGTGTGGAGCTGGACACAGCTGCGCT 228  
Db 189 GCGGACTGCGGCGGCGGAGCTGCGCAAGTGGGAGTGTGGAGCTGGACACAGCTGCGCG 248  
QY 229 GAGCAGCGGCTTTCCTTGGCGGCTCACCGCGGCGCT---CCTCGACTTCCCGCTGCGCG 285  
Db 249 GAGCAGCGGCTTTCCTTGGCGGCGGCTCGCGCGGCTCGCGCGCTCGCCATCTACTTCCCGCTGCGCG 308  
QY 286 GAGCGCGGAGCGAGCGGCGGAGTGGGACCGGCTTCCAGCGTGTGGCGGCTGCGCGCGCC 345  
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LOCUS AR177568 3911 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 1 from patent US 6312934.  
ACCESSION AR177568  
VERSION AR177568.1 GI:17919923  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3911)  
AUTHORS Johnson, G.L.  
TITLE Human MEK proteins, corresponding nucleic acid molecules, and uses thereof  
JOURNAL Patent: US 6312934-A 1 06-NOV-2001;  
FEATURES  
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ORIGIN  
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## RESULT 11

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AX803383 LOCUS 2103 bp DNA linear PAT 24-NOV-2003
DEFINITION Sequence 45 from Patent WO03000901.
ACCESSION AX803383
VERSION AX803383.1 GI:38502046
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Martinez, R.A. and Sigurdsson, G.T.
TITLES Nucleic acids encoding protein kinases
JOURNAL Patent: WO 03000901-A 45 03-JAN-2003;
Decode Genetics EHP. (US)
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## ORIGIN

Query Match 39.8%; Score 2086.8; DB 6; Length 2103;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2101; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

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[illegible]

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 DEFINITION Mus musculus MEK kinase mRNA, complete cds.  
 ACCESSION L3103  
 VERSION L3103.1 GI:293729  
 KEYWORDS MEK kinase.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 3244)  
 Lange-Carter, C.A., Pleiman, C.M., Gardner, A.M., Blumer, K.J. and  
 Johnson, G.L.  
 TITLE A divergence in the MAP kinase regulatory network defined by MEK  
 kinase and Raf  
 JOURNAL Science 260 (5106), 315-319 (1993)  
 MEDLINE 93227040  
 PUBMED 838502  
 COMMENT Original source text: Mus musculus (strain BALB/c, sub\_species  
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 mRNA.

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AUTHORS    Johnson,G.L.
TITLE       MEKK-related signal transduction kinases
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ORIGIN

Query Match 37.3%; Score 1955.6; DB 6; Length 3260;
Best Local Similarity 82.7%; Pred. No. 0;
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Qy      2776  TCAGAGACATTTCTGAGAGACTGGCCAGCATTTTCAGTAGGACCTTCTTAGTTCAACAACA 2835
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Qy      2836  ACAACAAACAACAACAGAGAACCAAGCCAAATGGTTCACAAACAAAGGACAGACCCAC 2895
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Qy      2896  AGTCAGTGTGTAACCTCTCTCTTTATCTCATCTTCCCAATTAATGTTTCCAGCCCTG 2955
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Qy      3256  GATCTGAACAGTAGTTCCTCAATGTATGATGACAGCTTTGGCTGTAGCAATAGTAGTAAT 3315
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Qy 4216 GAGTTTCAGGAGCAATTAATCTGGGAGCAATTTATGSCACCTGAGGTACTAAGAGT 4275  
Db 2175 GAGTTTCAGGAGCAATTAATCTGGGAGCAATTTATGSCACCTGAGGTACTAAGAGT 2234  
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ACCESSION AR085072  
VERSION AR085072.1 GI:10011843  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3260)  
AUTHORS Johnson,G.L.  
TITLES Methods for regulating MEKK protein activity  
JOURNAL Patent: US 5981265-A 1 09-NOV-1999;  
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Db 1 TACTACTCTTCCACAGCTTGGCAGAAAGAAATCAAACTTCAGAGACTTCTCCAGCCAGTT 60  
Qy 2056 GTAGACACCATCTCTAGTCAATGTGAGATGCCAATGCGGACCAAGTCAAGTCTGCTCCATA 2115  
Db 61 GTAGACACATCTCTTGTCAAGTGTGAGAT--CCAAACGCGGACAGTCAAGTCTGCTCCATA 119  
Qy 2116 TCACACACTGTGGAACTGTGCAAAAGGCAAGCAGGAGAGTGGCAGTTGGCAGAGAAATA 2175  
Db 120 TCTACAGTCTGGAACCTCTGCAAGGCGCCAGCAGGAGAGTGGCGGTTGGGAGAGAAATA 179  
Qy 2176 CTAAGAGCTGGAATCAATTTGATTTGGTGTGCTGATTAATTTGATTTCTTTGGA 2235  
Db 180 CTTAAAGCTGGGTCCATCGGGGTTGGTGTGCTGATTAATTTGATTTCTTTGGA 239







|    |      |                                                               |      |
|----|------|---------------------------------------------------------------|------|
| QY | 425  | CGGCCGAGCCGGGAGAAAGCGGGCGGCCCGCGAGCGCGTCTCTCTGAGCGGCCCGC      | 484  |
| DB | 362  | CGACCAGCCCGGGAGAAAGCGGGCGGCCCGCGCGCGCGCTCTCTCTGAGCGGCCCGC     | 421  |
| QY | 485  | CCGGTCTGAGATGGAGAAATAAGAAAACTCTCAAGGGTTGCAAGAATGATGATGTC      | 544  |
| DB | 422  | CCGGTCTGAGATGGAGAAATAAGAAAACTCTCAAGGGTTGCAAGAATGATGATGTC      | 481  |
| QY | 545  | CAGAGGAAAGAAATGATCAGGAGAAAACCTGAAGCAACTGTATGCCAGCTGGAAACAG    | 604  |
| DB | 482  | CAGGGAAAGAAATGATCAGGAGAAAACCTGAAGCAACTGTATGCCAGCTGGAAACAG     | 541  |
| QY | 605  | AATGTTGAAAAGGAGAAATAGCGAGGGCGCTGTGTGTATAAAACCAATCCAGTTAAAG    | 664  |
| DB | 542  | AATGTTGAAAAGGAGAAATAGCGAGGGCGCTGTGTGTATAAAACCAATCCAGTTAAAG    | 601  |
| QY | 665  | GAGATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCCAGGAGAGTCCAGGCAAGTG   | 724  |
| DB | 602  | GAGATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCCAGGAGAGTCCAGGCAAGTG   | 661  |
| QY | 725  | CGGTTTCAAGCTTCCAAAGGGCGAGCGAGTCTCTCTGGCACTCCCATCAGTCTC        | 784  |
| DB | 662  | CGGTTTCAAGCTTCCAAAGGGCGAGCGAGTCTCTCTGGCACTCCCATCAGTCTC        | 721  |
| QY | 785  | GCAGTGAATCAGAAATCTCCAGGAGTAGAGAGAAAAGAGTTTCCCAGTGCCTTTTC      | 844  |
| DB | 722  | GCAGTGAATCAGAAATCTCCAGGAGTAGAGAGAAAAGAGTTTCCCAGTGCCTTTTC      | 781  |
| QY | 845  | AGAGTGGCAATCAGACACCCGAGAGAGCCCTTCCAGAGTGCCTTCCACCATATA        | 904  |
| DB | 782  | AGAGTGGCAATCAGACACCCGAGAGAGCCCTTCCAGAGTGCCTTCCACCATATA        | 841  |
| QY | 905  | GCCCTGAGGAAAACAAACCGCGTGTAAACAAAGTGATCGGGCCAGACTGTACTTCTGC    | 964  |
| DB | 842  | GCCCTGAGGAAAACAAACCGCGTGTAAACAAAGTGATCGGGCCAGACTGTACTTCTGC    | 901  |
| QY | 965  | AGCAGATAGGCGCTAACTCTTTCTGATTTGGAGAGACAGCCAGACAAATAATACCGG     | 1024 |
| DB | 902  | AGCAGATAGGCGCTAACTCTTTCTGATTTGGAGAGACAGCCAGACAAATAATACCGG     | 961  |
| QY | 1025 | TGTTTATTTGGCCCTCAGAACTGCAGCTGTGCACGTGGAAATTTCTGTATTCATCTGCTAT | 1084 |
| DB | 962  | TGTTTATTTGGCCCTCAGAACTGCAGCTGTGCACATGGAATTTCTGTATTCATCTGCTAT  | 1021 |
| QY | 1085 | TTGTGATGCTCCGGGTGTTTCAACTAGAAAGCTTCAGACCCAAATGTTATGGAGAAAACCT | 1144 |
| DB | 1022 | TTGTGATGCTCCGGGTGTTTCAACTAGAAAGCTTCAGACCCAAATGTTATGGAGAAAACCT | 1081 |
| QY | 1145 | TAAAGAAATTTTGGGTTGAGAGTTTGTTCAGAAATATCAGTAGGCGTAGCTCAAGGA     | 1204 |
| DB | 1082 | TAAAGAAATTTTGGGTTGAGAGTTTGTTCAGAAATATCAGTAGGCGTAGCTCAAGGA     | 1141 |
| QY | 1205 | TCAAAGCTCCATCTGCTGTAACCAATCAGAAAGTTGTTTCCAGCATGTCAAAATCTCATA  | 1264 |
| DB | 1142 | TCAAAGCTCCATCTGCTGTAACCAATCAGAAAGTTGTTTCCAGCATGTCAAAATCTCATA  | 1201 |
| QY | 1265 | CATTGTCATCATCTAGTACTTCTACGTTCCAGAAAACAGCATAAAGGATCAAGAGG      | 1324 |
| DB | 1202 | CATTGTCATCATCTAGTACTTCTACATCTAGTTCCAGAAAACAGCATAAAGGATCAAGAGG | 1261 |
| QY | 1325 | AACAGATGTGCTTATTTGCTTTGTTGGCATGCTTGTATGAAGAAAGTCTTACAGTGTGTC  | 1384 |
| DB | 1262 | AACAGATGTGCTTATTTGCTTTGTTGGCATGCTTGTATGAAGAAAGTCTTACAGTGTGTC  | 1321 |
| QY | 1385 | AAGACGGCTGACAGGAAACAGCTGCACCACTGCATGTCAATTTGGGCGAAGAGTGTA     | 1444 |
| DB | 1322 | AAGACGGCTGACAGGAAACAGCTGCACCACTGCATGTCAATTTGGGCGAAGAGTGTA     | 1381 |
| QY | 1445 | GAAGAAATAGAGAAACCTTTTATATGTCCCTTTGTAGATCTTAAGTGGAGATCTCATGATT | 1504 |
| DB | 1382 | GAAGAAATAGAGAAACCTTTTATATGTCCCTTTGTAGATCTTAAGTGGAGATCTCATGATT | 1441 |

|    |      |           |              |            |                |                        |                           |      |
|----|------|-----------|--------------|------------|----------------|------------------------|---------------------------|------|
| QY | 1505 | TCTACAGCA | CGAGTGTG     | CTCAAGT    | CTCTGTGGAT     | TCCCTCTCT              | CTCCCTCAGAGCTGCACAGC      | 1564 |
| DB | 1442 | TCTACAGCA | CGAGTGTG     | CTCAAGT    | CTCTGTGGAT     | TCCCTCTCT              | CTCCCTCAGAGCTGCACAGC      | 1501 |
| QY | 1565 | AGCAAA    | CCGCTACAGCA  | CGAGCTTT   | GGCTGGAT       | CAAGAGGAAT             | CAAGAGAGCAATTTTA          | 1624 |
| DB | 1502 | AGCAAA    | CCGCTACAGCA  | CGAGCTTT   | GGCTGGAT       | CAAGAGGAAT             | CAAGAGAGCAATTTTA          | 1561 |
| QY | 1625 | ACCTTACT  | CATTATG      | GAATCTCA   | GCAAAATCCCT    | CTGCTTACAAAGATTT       | TAGCTGAGCCAT              | 1684 |
| DB | 1562 | ACCTTACT  | CATTATG      | GAATCTCA   | GCAAAATCCCT    | CTGCTTACAAAGATTT       | TAGCTGAGCCAT              | 1621 |
| QY | 1685 | GGATT     | CAGTGTGTT    | TGGAATG    | GAATCTCGT      | TGGCTGCTTATTTCT        | TAGAACTCGGAATGTGA         | 1744 |
| DB | 1622 | GGATT     | CAGTGTGTT    | TGGAATG    | GAATCTCGT      | TGGCTGCTTATTTCT        | TAGAACTCGGAATGTGA         | 1681 |
| QY | 1745 | GAGAGAT   | GCGCCCTCAG   | CGCTCTTTCC | CAATGATCTCAGT  | GCGGCCCTCTGTTGGCAAAATG | 1804                      |      |
| DB | 1682 | GAGAGAT   | GCGCCCTCAG   | CGCTCTTTCC | CAATGATCTCAGT  | GCGGCCCTCTGTTGGCAAAATG | 1744                      |      |
| QY | 1805 | GGGAGAGCA | CTGGAATTTCT  | GCGGGCAG   | CAGTGGAAAGCAG  | CGCGAGTGGGGGAGCCACCA   | 1864                      |      |
| DB | 1742 | GGGAGAGCA | CTGGAATTTCT  | GCGGGCAG   | CAGTGGAAAGCAG  | CGCGAGTGGGGGAGCCACCA   | 1801                      |      |
| QY | 1865 | GTGGTCT   | CTCCAGAC     | CCAGTATCT  | CAGGAGATGTG    | TGTGGAGGCAU            | CTGTCAGCGTCTCTGT          | 1924 |
| DB | 1802 | GTGGTCT   | CTCCAGAC     | CCAGTATCT  | CAGGAGATGTG    | TGTGGAGGCAU            | CTGTCAGCGTCTCTGT          | 1861 |
| QY | 1925 | CAAT      | TGCTGTG      | CTGAC      | CCCTGTCTCA     | AAAGTGTAC              | GTGTGCTTTTAAAAACATTTGAGAG | 1984 |
| DB | 1862 | CAAT      | TGCTGTG      | CTGAC      | CCCTGTCTCA     | AAAGTGTAC              | GTGTGCTTTTAAAAACATTTGAGAG | 1921 |
| QY | 1985 | CCAT      | GTCTGTATATAC | TCTCTTGG   | CCAGTTTAC      | GCGGAAGAAATCAAACTTT    | CAGAGACTTC                | 2044 |
| DB | 1922 | CCAT      | GTCTGTATATAC | TCTCTTGG   | CCAGTTTAC      | GCGGAAGAAATCAAACTTT    | CAGAGACTTC                | 1981 |
| QY | 2045 | TCCAG     | CAAGTGTG     | TAGACAC    | CAATCTTAGT     | CAAAATGTG              | CGCATAGCCGCACAGTC         | 2104 |
| DB | 1982 | TCCAG     | CAAGTGTG     | TAGACAC    | CAATCTTAGT     | CAAAATGTG              | CGCATAGCCGCACAGTC         | 2041 |
| QY | 2105 | AGCTGT    | CCATATCA     | CAACTGT    | TGGAATCTG      | CAAAAGGCCAAGCAGGAGAGT  | TGGCAGTTG                 | 2164 |
| DB | 2042 | AGCTGT    | CCATATCA     | CAACTGT    | TGGAATCTG      | CAAAAGGCCAAGCAGGAGAGT  | TGGCAGTTG                 | 2101 |
| QY | 2165 | GCAGAGAA  | ATACTTAA     | AGCTGGAT   | TCCATTTGGTAT   | TGGTGTGTGAT            | TGTTTAAAT                 | 2224 |
| DB | 2102 | GCAGAGAA  | ATACTTAA     | AGCTGGAT   | TCCATTTGGTAT   | TGGTGTGTGAT            | TGTTTAAAT                 | 2161 |
| QY | 2225 | GTA       | TTCTTGGAAA   | CCAAACTGA  | ATCAAACTTTGG   | CAAGAACTCTTTGG         | CGCGCTTTGTC               | 2284 |
| DB | 2162 | GTA       | TTCTTGGAAA   | CCAAACTGA  | ATCAAACTTTGG   | CAAGAACTCTTTGG         | CGCGCTTTGTC               | 2221 |
| QY | 2285 | TTATAGAT  | AGACTGT      | TGTTGGA    | ATTTCCCTGCTG   | GAATTTATCTCATAT        | TGTCAGTACTG               | 2344 |
| DB | 2222 | TTATAGAT  | AGACTGT      | TGTTGGA    | ATTTCCCTGCTG   | GAATTTATCTCATAT        | TGTCAGTACTG               | 2281 |
| QY | 2345 | ATG       | TTTCA        | CAAGCTGAG  | CGCTGTTGAAAT   | CAGSTATAGAA            | AGCTGCTGCTCTTTAA          | 2404 |
| DB | 2282 | ATG       | TTTCA        | CAAGCTGAG  | CGCTGTTGAAAT   | CAGSTATAGAA            | AGCTGCTGCTCTTTAA          | 2341 |
| QY | 2405 | TTGCTTT   | TCAGTCCA     | TTTGAT     | AAATTTCCCACTCA | ATGTTGGCAAACTTT        | TCAGAGAGGATCT             | 2464 |
| DB | 2342 | TTGCTTT   | TCAGTCCA     | TTTGAT     | AAATTTCCCACTCA | ATGTTGGCAAACTTT        | TCAGAGAGGATCT             | 2401 |
| QY | 2465 | ACTT      | CAGTCTCTG    | CAAGAAATG  | GTATCTACAGT    | TACCCCAATGTGTTTT       | CAAACTGTTAGAAA            | 2524 |
| DB | 2402 | ACTT      | CAGTCTCTG    | CAAGAAATG  | GTATCTACAGT    | TACCCCAATGTGTTTT       | CAAACTGTTAGAAA            | 2461 |
| QY | 2525 | TGCT      | CAGTGTTC     | CAG---     | TTTCCACTCACTT  | CAACAGGATCGCT          | CGCGTTTGATGGCTA           | 2581 |
| DB | 2462 | TGCT      | CAGTGTTC     | CAG---     | TTTCCACTCACTT  | CAACAGGATCGCT          | CGCGTTTGATGGCTT           | 2521 |
| QY | 2582 | TTG       | CAAGATGAG    | TGGAATTTG  | CCGAAGCCAT     | CTCAGTTGGGCGT          | TAGAAGACATTTGGATG         | 2641 |

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Qy 3599 CTCAGGATGCTCCCTCCATAGTTCTCTCAGCTGAGGTTGAAAATGGAGAGATATCATCA 3658  
Db 3542 CTCAGGATGCTCCCTCCATAGTTCTCTCAGCTGAGGTTGAAAATGGAGAGATATCATCA 3601  
Qy 3659 TTATTCAACAGGATACACAGAGACTCTTACAGGACATACCAAGCAAAACACCGTATA 3718

Db 3602 TTATTCAACAGGATACACAGAGACTCTTACCAGGACATACCAAGCAAAACACCGTATA 3661  
Qy 3719 GAGAAGACACTGAATGGCTGAAAGGTCAACACATAGGCTTCGAGCAATTTCTTCTTGT 3778  
Db 3662 GAGAAGACACTGAATGGCTGAAAGGTCAACACATAGGCTTCGAGCAATTTCTTCTTGT 3721  
Qy 3779 ATCAGGCTCAAGATGCGGAACCTGGAACCTTTAATGGCTGTTAAACAGGTGACTTATGTCA 3838  
Db 3722 ATCAGGCTCAAGATGCGGAACCTGGAACCTTTAATGGCTGTTAAACAGGTGACTTATGTCA 3781  
Qy 3839 GAAACACATCTTCTGAGCAAGAAAGTAGTAGAAGCACTAAGAGAGAGAGATAAGAAATCA 3898  
Db 3782 GAAACACATCTTCTGAGCAAGAAAGTAGTAGAAGCACTAAGAGAGAGAGATAAGAAATCA 3841  
Qy 3899 TGAGCCATCTGAATCTATCCAAACATATTAGATGTTGGAGCCACCTGTGAGAGAGCA 3958  
Db 3842 TGAGCCATCTGAATCTATCCAAACATATTAGATGTTGGAGCCACCTGTGAGAGAGCA 3901  
Qy 3959 ATTACAAATCTCTTCAATTTGAATGGATGGCAGGGGGATCGGTGCTCATTTGCTGAGTAAT 4018  
Db 3902 ATTACAAATCTCTTCAATTTGAATGGATGGCAGGGGGATCGGTGCTCATTTGCTGAGTAAT 3961  
Qy 4019 ATGAGCCCTTCAAGAAATCAGTAGTTTAACTACACTGAAACAGTTACTCCGTGGCTTT 4078  
Db 3962 ATGAGCCCTTCAAGAAATCAGTAGTTTAACTACACTGAAACAGTTACTCCGTGGACTTT 4021  
Qy 4079 CGTATCTCCATGAAACCAAAATCATTTACAGAGATGTCAAAGGTGCCAATTTGCTAATTTG 4138  
Db 4022 CGTATCTCCATGAAACCAAAATCATTTACAGAGATGTCAAAGGTGCCAATTTGCTAATTTG 4081  
Qy 4139 ACAGCACTGGTACAGACATAAGAAATTTGGAGCTGCGAGCGAGTTGGCATCAA 4198  
Db 4082 ACAGCACTGGTACAGACATAAGAAATTTGGAGCTGCGAGCGAGTTGGCATCAA 4141  
Qy 4199 AAGGAAGCTGGTACAGAGAGTTTACAGGACAAATCTGCGGACAAATTTGCAATTTATGGCAC 4258  
Db 4142 AAGGAAGCTGGTACAGAGAGTTTACAGGACAAATCTGCGGACAAATTTGCAATTTATGGCAC 4201  
Qy 4259 CTGAGGTACTAAGAGGTCAACAGTATGGAAGGAGCTGTGATGTATGAGAGTTGGCTGTG 4318  
Db 4202 CTGAGGTACTAAGAGGTCAACAGTATGGAAGGAGCTGTGATGTATGAGAGTTGGCTGTG 4261  
Qy 4319 CTATTTAGAAATGGCTTGTGCAAAACCAACCCAGTGAATGCAGAAAACCACTCCCAATCATC 4378  
Db 4262 CTATTTAGAAATGGCTTGTGCAAAACCAACCCAGTGAATGCAGAAAACCACTCCCAATCATC 4321  
Qy 4379 TTGCTTTGATTTTAAAGATTGCTAGTGCAACTACTGCTCCATCGATCCCTTCAATTTGT 4438  
Db 4322 TTGCTTTGATTTTAAAGATTGCTAGTGCAACTACTGCTCCATCGATCCCTTCAATTTGT 4381  
Qy 4439 CTCCTGGTTTACAGAGTGGCTCTTGGTTGTTTAGAACTTCAACCTCAGGACAGACCTC 4498  
Db 4382 CTCCTGGTTTACAGAGTGGCTCTTGGTTGTTTAGAACTTCAACCTCAGGACAGACCTC 4441  
Qy 4499 CATCAAGAGAGCTACTGAAGCATCCAGTCTTTCGTACTACATGATGATGATGATGATGATGAT 4558  
Db 4442 CATCAAGAGAGCTACTGAAGCATCCAGTCTTTCGTACTACATGATGATGATGATGATGATGAT 4501  
Qy 4559 TCAACTACAGTAGAAGACAGGATGCTCAACAGAGAAAAAATACTTGTGGGAAACCACTT 4618  
Db 4502 TCAACTAC-GTAGAAACAGGATGCTCAACAGAGAAAAAATACTTGTGGGAAACCACTT 4560  
Qy 4619 GATATTCTACTGCGCATGATGCCACTGAACAGCTATGAACAGGCGCAGTGGGAAACCTT 4678  
Db 4561 GATAT--CTAGGCGCATGATGCCACTGAACAGCTATGAACAGGCGCAGTGGGAAACCTT 4618  
Qy 4679 ACCTAAGTATGATTTGACAAATCATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 4738  
Db 4619 ACCTAAGTATGATTTGACAAATCATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 4678  
Qy 4739 ACTAGTCAGAAACT 4753  
Db 4679 ACTAGTCAGAAACT 4693



RESULT 2  
US-09-423-890-7  
; Sequence 7, Application US/09423890  
; Patent No. 6312934  
; GENERAL INFORMATION:  
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION  
; TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: CPI-085CPC  
; CURRENT APPLICATION NUMBER: US/09/423,890  
; CURRENT FILING DATE: 2000-03-06  
; PRIOR APPLICATION NUMBER: USN 60/078,153  
; PRIOR FILING DATE: 1998-03-16  
; PRIOR APPLICATION NUMBER: USN 60/099,165  
; PRIOR FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 5253  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (15)..(4493)  
US-09-423-890-7

Query Match 65.1%; Score 3417; DB 4; Length 5253;  
Best Local Similarity 83.5%; Pred. No. 0;  
Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;

|    |     |                                                               |     |
|----|-----|---------------------------------------------------------------|-----|
| QY | 1   | GAGAAATCGCGCGCGCGGGAATCGCCTCGTCGTCGGGATTCGCGGCGCCAGG          | 60  |
| DB | 9   | GAGAAATCGCGCGCGCGGCGGCGATCGCCTCGTCGTCGGGATTCGCGGCGCCAGG       | 68  |
| QY | 61  | GCTACGAGCCCTGAGCAGCGCGCGGC-----GAGAGAGCCCTCAAGCGAGCAGC        | 111 |
| DB | 69  | GCGGCGAGTCCCGAGCGCGCGCGCGCGCGCGCGGAGGAGGAGCTCTCCAGGAAAGCGCG   | 128 |
| QY | 112 | GGGCCC---GGCGCTCGCGGAGCTGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCG       | 168 |
| DB | 129 | GCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG       | 188 |
| QY | 169 | GCAGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG      | 228 |
| DB | 189 | GCAGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG      | 248 |
| QY | 229 | GAGCAGCGCTCTTCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG     | 285 |
| DB | 249 | GAGCAGCGCTCTTCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG     | 308 |
| QY | 286 | GAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG    | 345 |
| DB | 309 | GAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG    | 368 |
| QY | 346 | CAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG    | 405 |
| DB | 369 | CGCGGAGCGCGAGTGCCTCGCGCTCCCACTCTGCGGAGTGGCGCGCGCGCGCGCGCGCG   | 428 |
| QY | 406 | GGCGCTTCGAGTCCCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG   | 465 |
| DB | 429 | GGCGCTTCGAGTCCCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG   | 458 |
| QY | 466 | TCTCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG  | 525 |
| DB | 459 | CCCTCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG | 518 |
| QY | 526 | CACAGATGGATGATCGTCCAGAGCAACGAATGATCAGGAGGAACTGAAAGGCAACTGT    | 585 |
| DB | 519 | CACAGATGGAGGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG  | 578 |
| QY | 586 | ATGCCAGCCTGGAAGCAGCAATGTTGTAAGAGGAGAAATAGGCGAGGCGCTGTGGTGGTA  | 645 |

|    |      |                                                                 |      |
|----|------|-----------------------------------------------------------------|------|
| DB | 579  | ATGCCAGCCTGGAAGCAGCAATGTTGTAAGAGGAGAAACAGAGAGGCGCTGTGGTGGTG     | 638  |
| QY | 645  | AAACCAATCCAGTAAAGGAGATGATCTGAATGAATCACTTAGCAGCTGAGTCTCCA        | 705  |
| DB | 639  | AAAGCAATCCCTATTAAAGGAGATGATCTGAAGTGAATAAATTTGGCAGCTGAGCCAG      | 698  |
| QY | 706  | GAGAGGTCAGGCAAGTGGCGCTTCCAGAGTCCAAAGCGCGCAGCAGCTCTCTCTCT        | 765  |
| DB | 699  | GAGAGGTCAGGCAAGTGGCGCTTCCAGAGTCCAAAGCGCGCAGCAGCTCTCTCTCT        | 758  |
| QY | 766  | GGCAATCCCTCAGTTCAGCTCGCAGTGAATCTCCAGGAGTGAAGAGAAAGA             | 825  |
| DB | 759  | GGCAGCTCTCCCTCAGGCGCTCGGTGAAGCGGAAATCCCGAGGAGTGAAGAGAAAGA       | 818  |
| QY | 826  | GTTCCTCCAGTGGCTTTTCAGAGTGGCAGAAATCACACACCCCGAGAGCGCTTCAACA      | 885  |
| DB | 819  | GTTCCTCCAGTGGCTTTTCAGAGTGGCAGAAATCACACACCCCGAGAGCGCTTCAACA      | 878  |
| QY | 886  | GATGGCTTCTCACCATATAGCCCTGAGGAAACAAACCCGCGCTTTAAACAAAGTGTGGG     | 945  |
| DB | 879  | GATGGCTTCTCACCATATAGCCCTGAGGAAACAAACCCGCGCTTTAAACAAAGTGTGGG     | 938  |
| QY | 946  | GCCAGACTGTACTTACTGAGCAGATAGGCGCTTAATCTTCTCTGATTTGGAGGAGCAGC     | 1005 |
| DB | 939  | GCCAGACTGTACTTACTGAGCAGATAGGCGCTTAATCTTCTCTGATTTGGAGGAGCAGT     | 998  |
| QY | 1006 | CCAGACAATAATACCGGCTGTTTATTTGGGCTTCAGAACTGCAGCTGTGCACGTGAAACA    | 1065 |
| DB | 999  | CCAGACAATAATACCGGCTGTTTATTTGGGCTTCAGAACTGCAGCTGTGCAGGAGCA       | 1058 |
| QY | 1066 | TTCTGATTCATGCTATTTGATGCTCCGCGTGTTCCTCTGATTTGGAGGAGCAGC          | 1125 |
| DB | 1059 | TTCTGATTCATGCTATTTGATGCTCCGCGTGTTCCTCTGATTTGGAGGAGCAGC          | 1118 |
| QY | 1126 | ATGTTTGGAGGAAACTTTTAAAGAAATTTGAGTTTGAGAGTTTGTTCAGAAATATCAC      | 1185 |
| DB | 1119 | ATGTTTGGAGGAAACTTTTAAAGAAATTTGAGTTTGAGAGTTTGTTCAGAAATATCAC      | 1178 |
| QY | 1186 | AGTAGGCTGAGCTCAAGGATCAAGCTCCATCTCGTAAACCAATCCAGAGTTTGTTC        | 1245 |
| DB | 1179 | AGTAGGCTGAGCTCAAGGATCAAGCTCCATCTCGTAAACCAATCCAGAGTTTGTTC        | 1238 |
| QY | 1246 | CGCATGCAATTTCTCATACATTTGTATCTTCTACTTCTACTCTTCTAGTTCAGAAAC       | 1305 |
| DB | 1239 | CGCATGCAATTTCTCATACATTTGTATCTTCTACTTCTACTCTTCTAGTTCAGAAAC       | 1298 |
| QY | 1306 | AGCAATGAAGTGAAGAGGAAACAGATGTGCTTCTTCTTGTGGCATGCTTGTATGA         | 1365 |
| DB | 1299 | AGCATGAAGTGAAGAGGAGGATGTGCTTCTTCTTGTGGCATGCTTGTATGA             | 1358 |
| QY | 1366 | GAAAGTCTTACAGTGTGAGAGCGGCTGCAGGAAACAGCTGCACCACTGCATGTCA         | 1425 |
| DB | 1359 | GAAAGTCTTACAGTGTGAGAGCGGCTGCAGGAAACAGCTGCACCACTGCATGTCC         | 1418 |
| QY | 1426 | ATTTGGGAGAGTGTAGAGAAATAGAGAACTTTTAAATATGTCCCTTTGTAGATCT         | 1485 |
| DB | 1419 | ATTTGGGAGAGTGTAGAGAAATAGAGAACTTTTAAATATGTCCCTTTGTAGATCT         | 1478 |
| QY | 1486 | AAGTGGAGATCTCATGATTTCTACAGCAGAGTTGCAAGTCTCTGTGGATTCCTCTTCT      | 1545 |
| DB | 1479 | AAGTGGAGATCTCATGATTTCTACAGCAGAGTTGCAAGTCTCTGTGGATTCCTCTTCT      | 1538 |
| QY | 1546 | TCCCTTCAGAGTGCACAGCAGCAACCGTACAGCAGAGCTTTGGGTGGATCA---CGA       | 1602 |
| DB | 1539 | TCCCTTCAGAGTGCACAGCAGCAACCGTACAGCAGAGCTTTGGGTGGATCA---CGA       | 1598 |
| QY | 1603 | AGGAATCAAGAGAGCAATTTTAACTTACTTATGGAATCTCAGCAATCCCTCTCTCT        | 1662 |
| DB | 1599 | AGGAATCAAGAGAGCAATTTTAACTTACTTATGGAATCTCAGCAATCCCTCTCTCT        | 1658 |
| QY | 1663 | TACAAAGATTTAGCTGAGCCATGAGTTCAGTGTTCAGATGGAATGGAATCTGTTGGCTGCTTA | 1722 |

Db 1659 TACAAAGATTTGGCGAGCCATGGATTACAGTGTGTTGGAATGGAACTCGTTGGCTGCTTA 1718  
Qy 1723 TTTTCTAGAACTGGAATGTGAGAGATGCGCCCTCAGGGCTCTTTCCCATGATGTCAGT 1782  
Db 1719 TTCTCTAGAACTGGAATGTGAGAGATGCGCCCTCAGGGCTCTTTCCCATGATGTCAGT 1778  
Qy 1783 GGGGCCCTGCTGTTGGCAAAATGGGAGAGCACTGGAATTTCTGGGGCAGCAGTGGGAAGC 1842  
Db 1779 GGGGCCCTGTTGTTGGCAAAATGGGAGAGCACTGGAATTTCTGGGGCAGCAGTGGGGGC 1838  
Qy 1843 AGCCGAGTGGGGAGCCACAGTGGGTCTTCCAGAGCCAGTATCTCAGGAGATGTGGTG 1902  
Db 1839 AGCTTAAGCGGGAGCGCCAGCGGTCTTCCAGCCAGCATCTCAGGGGATGTGGTG 1898  
Qy 1903 GAGCATGCTCAGCGTTCTCTCAATGTCTGTGCTGACCTGTCTCAAGTGTACGTT 1962  
Db 1899 GAGCGTCTCAGTGTCTCTCTATAGTCTGCGCTGACCTGTCTCAAGTGTACGTT 1958  
Qy 1963 GCTGCTTTAAAAACATTTAGAGGCCATGCTGGTATATATCTCTGCCACAGTTTAGCGAA 2022  
Db 1959 GCTGCTTTAAAAACATTTAGAGGCCATGCTGGTATATATCTCTGCCACAGTTTAGCGAA 2018  
Qy 2023 AGAATCAAACTTCAGAGACTCTCCAGCCAGTGTGAGACACCATCTAGTCAAAATGCA 2082  
Db 2019 AGAATCAAACTTCAGAGACTCTCCAGCCAGTGTGAGACACCATCTAGTCAAAATGCA 2078  
Qy 2083 GATGCCAATAGCCGACAAAGTCACTGTCCATATCAACACACTGTGTGGAACTGTGCAAAAGGC 2142  
Db 2079 GATGCCAACACCGCACAGTCACTGTCCATATCTACAGTGTGGAACTGTGCAAAAGGC 2138  
Qy 2143 CAGCAGGAGAGTGTGGAGTGTGGCAGAGAAATATCAAAAGCTGGATCAATGTGTTGGT 2202  
Db 2139 CAAGCAGGAGAGTGTGGAGTGTGGCAGAGAAATATCAAAAGCTGGATCAATGTGTTGGT 2198  
Qy 2203 GGTGTGATATGCTTAAATTTGATTTCTTGAAACCAAACTGAAATCAAACTGGCAA 2262  
Db 2199 GGTGTGATATGCTTAAATTTGATTTCTTGAAACCAAACTGAAATCAAACTGGCAA 2258  
Qy 2263 GAACTTCTTGGCGCTTGTCTTATAGATAGATGTTGTTGGAAATTTCTGCTGAATTT 2322  
Db 2259 GAACTTCTTGGCGCTTGTCTTATAGACAGTGTGTTGGAAATTTCTGCTGAATTT 2318  
Qy 2323 TATCTCTATATGTCAGTACTGATGTTTACAGCTGAGCTGTTGAAATCAGGTATTAAG 2382  
Db 2319 TATCTCTATATGTCAGTACTGATGTTTACAGCTGAGCTGTTGAAATCAGGTATTAAG 2378  
Qy 2383 AAGCTGCTCCCTCTTAACTTTGCTTTGAGTCCATGATTAATTTCCCACTCAATGTT 2442  
Db 2379 AAGCTGCTCCCTCTTAACTTTGCTTTGCAATCCATGCAATTTCCCACTCAATGTT 2438  
Qy 2443 GGCNAATTTCCAGAGGATCTACTGATTTCTGCAAGATGTTTACTACAGTACCCCAT 2502  
Db 2439 GGCNAAGCTCTCTCGGAGGATATATCTGAGCTCTGCAAGATGTTGACCGAGTGTCCCGCT 2498  
Qy 2503 GTGTTTTCAAAACATGTTAGAAATGCTGAGTGTTCAGTTCACCTCACTTCCACAGGATG 2562  
Db 2499 GTGTTTTCAAAACATGTTAGAAATGCTGAGTGTTCAGTTCACCTCACTTCCACAGGATG 2558  
Qy 2563 CGTCGCGCTTGTGATGCTATGCAATGAGTGTGAAATTTGCCAGAGCCATCCAGTGTGGC 2622  
Db 2559 CGCGCGCTGCTGATGCTATGCGGATGAGTGTGAAATTTGCCAGAGTCACTCAGCTGGT 2618  
Qy 2623 GTAGAGACACTTTGGATGCTCAACAGGACAGCTTCTTCCAGGCACTGTGTTCCCAACAC 2682  
Db 2619 GTGGAGGACACTGTGATGGGATCAGGACAG ---CTTACAGCGCTGGCCCCCACCAGC 2675  
Qy 2683 TATCTGGAAACCAAGAGAACAGTTCCTCTGAGTGTGACAGTCCATTTAGAGAAATCTGGA 2742  
Db 2676 TGTCT -----AGAAACAGCTCCCTTGGAGCAACAGTCCATAGAGAGAAATCTGGA 2726  
Qy 2743 AAAGGATTTATGCTCAAAATTTGAGTCCAGTTTCAAGAGCAATTTCTCAGAGACTGGCC 2802  
Db 2727 AAAGGACTAAGTCTCAGGACTGAGTCCAGCTCGAGGACATTTCTCAGACAGTGGCC 2786

Qy 2803 AGCATTTCTAGTAGGACCTTCTAGTTTCAACAACAACAACAACAACAACAACAACAACA 2862  
Db 2787 GCGCTCTCTGTAGGACTTCCAGCT -----CAACAACAACAACAACAACAACAACA 2831  
Qy 2863 AAGCCAAATGTTTCAAAACAAAAGGAGAGCCCAACAGTCTAGTGTGTTGAATCTCTCTTTA 2922  
Db 2832 AAGCCAGCGTTTCAAAACAAAAGGAGAGCCCAACAGTCTAGTGTGTTGAATCTCTCTCTTTG 2891  
Qy 2923 TCTCATCATTCGAATTAATGTTTCAGGCTTGTCAAACCCCTCTCTCTTACCCCATCT 2982  
Db 2892 TC ---TCATGCTCAATTAATGTTTCGAGCACCATCAGCCCTTGTTCCTCTGCCCCGCT 2948  
Qy 2983 GTACCAGCTGGCACTGCAACAGATGCTCTAAGCATAGACTTTCAGGGAATTCATTCCTGTC 3042  
Db 2949 GTCC -----CAGATATTCTAAGCAGACACCCAGGCAATTTGTTCCCTGTC 2993  
Qy 3043 AGAATACCTTCTGATCTCTCTCAACAACAGCCGAAGTTTCTCTACAAATTCACAGAAAC 3102  
Db 2994 AATAATACCTTTCGCACTCTCTCAGACACAGCCGAAGTTTCTCTACAAATTCAGAGGAAC 3053  
Qy 3103 TGTCTTGA AAAACAAAAGACTCAGATAAACTTTCCCAAGTCTTTTACTCAGTCAAGAGCCCTTG 3162  
Db 3054 TGTCTTGAACAACCGAGACTCAGACAGCTCTCCCAAGTCTTCTCTCAGTCAAGACCCCA 3113  
Qy 3163 CCGCTCAGTAACATACACAGGCCAAGCCATCTAGACCTACCCAGTGTAAATCAAGTAA 3222  
Db 3114 CCGCTCAGTAACATACACAGGCCAAGCCATCTCCCAAGTCTTCCGGGAGTACAGCAAA 3173  
Qy 3223 CAGGGAGATCCCTCAAAAATAGCATGACACTGTGATCTGAAACAGTAGTTCCAAATGTGAT 3282  
Db 3174 CTAGGGAGGCCA AAAAGTGTAGTACACTGTGATCTGGGAGTCTTCCAGGTGTGAC 3233  
Qy 3283 GACAGCTTTGGCTGTAGCAGCAATAGTAAATGCTGTGTTATACCCAGTGAAGAGCAGTG 3342  
Db 3234 GACAGCTTTGGCGCGCGCAACAGTGGCAACCGCTCATACCCAGCGACGAGCAGTG 3293  
Qy 3343 TTCACCCAGTAGAGGAATGCGAGATGATGATGATGATGATGATGATGATGATGATGAT 3402  
Db 3294 TTCACCGCGTGAGGAGCAAGTGCAGTGTAGTGTGAAACCGAGTCACTTCCAGCATC 3353  
Qy 3403 GAGGACCTTCTTGAAGCATCTATGCTTCAAGTGATACAAACAGTAACTTTTAAAGTCAGAA 3462  
Db 3354 GAGGACCTTCTTGAAGCATCTATGCTTCAAGTGATACAAACAGTCACTTTCAGTCCGAA 3413  
Qy 3463 GTTGTGCTCTCTCTGAAAGGCTGAAATGATGATGATGATGATGATGATGATGATGAT 3522  
Db 3414 GTCCCGTCTCTCTCTCGGAAAGGCGGAAATGAGCAGCACCCTTACAAAGACGCTCAAT 3473  
Qy 3523 CATAAATCAAAAGTGC AAAAGAGATGGAAGCTGGAAGAGAGAGAGAGAGAGAGAGAG 3582  
Db 3474 CATAAATCAAAAGTGC AAAAGAGATGGAAGCTGGAAGAGAGAGAGAGAGAGAGAG 3533  
Qy 3583 ATGGCAATGTCAAGGTCTCAGGATGCGCTCCCATAGTTCCTCAGTGTGAGGTTGAAAT 3642  
Db 3534 ATGGCAATGTCAAGGTCTCAGGATGCGCTCCCATAGTTCCTCAGTGTGAGGTTGAAAT 3593  
Qy 3643 GGAGAGATATCATATTATTCAACAGGATACACAGAGACTCTACAGGACATACCAAA 3702  
Db 3594 GGAGAGATATATCATATTATTCAACAGGACACACAGAACTCTTCCAGGACATACCAAA 3653  
Qy 3703 GC AAAACAAACCGTATAGAGAAACACTGAATGCTGAAAGGTCAAACGATAGGCTTGGGA 3762  
Db 3654 GCGAAAACAGCTTACAGAGAAAGCGCTGAGTGTCTGAAAGGCCAGCAGATAGGCTTGGGA 3713  
Qy 3763 GCATTTTCTTCTTGTATCAGGCTCAAGATGTGGAACTGGAATTTTAAATGGCTGTAAAA 3822  
Db 3714 GCATTTTCTTCTTGTATACCAAGCAGGATGTGGGACTGGGACTTTAAATGGCTGTAAA 3773  
Qy 3823 CAGGTGATTTATGTCAAAAACATCTTCTGAGCAGAAAGAGTGTGTAGAGCACTAAGA 3882  
Db 3774 CAGGTGACGTACGTCAAAAACATCTCTCCGAGCAGGAGAGGTGTGTGGAAGGTTGAGG 3833



Db 866 TGCCGGCCTGGAAAGCAAGAGTGGTTGGAGAGAGGAAACAGAGAGGCCCTGTGGTGGTGA 925  
Qy 647 AACCAATCCCAAGTTAAAGGAGATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCCAG 706  
Db 926 AGCCAAATCCCTATTAAAGGAGATGGATCTGAAATGAATCACTTAGCAGCTGAGCCCAAG 985  
Qy 707 GAGAGTCCAGCAAGTCCGCTTCAACAGCTTCCAAAGCCGACGAGTCCCTCTCTCTG 766  
Db 986 GAGAGGCGCAGGCAAGTTCGCTGCACAGCCCCCAAGGGCCGACGAAGCCCATCTCTCTG 1045  
Qy 767 GCAATCCCCATCAGGTCGACAGTGAATCTCCAGGAGTAAAGGAGAAAGAG 826  
Db 1046 GCAGCTCTCCGTCAGGCGCTCGGTGAAGCCGGAATCCCCAGGAGTAAAGCGGAACGAG 1105  
Qy 827 TTTCCCAAGTCCCTTTTCAGAGTGGCAGAAATCACACACCCCGAAGAGCCCTTCCAG 886  
Db 1106 TGTCCCGGTCCTTTCCAGAGTGGCAGAAATCACACACCCCGAAGAGCCCTTCCAG 1165  
Qy 887 ATGGCTTCTCAACATATAGCCCTCAGGAAACAAACCGCGCTGTAAACAAAGTGAATGCGGG 946  
Db 1166 ATGGCTTCTCCCGTACAGCCAGAGAGACGAGCGCGCGTGAACAAAGTGAATGAGAG 1225  
Qy 947 CCAGACTACTTACTCAGCAGATPAGGGCCCTAACTCTTCTCTGATTTGGAGAGACAGCC 1006  
Db 1226 CCAGCTGTACTGTCTGAGCAGATPAGGACCACTCTTCTCTGATTTGGAGAGACAGTC 1285  
Qy 1007 CAGACAAATAATACCGGTGTTTATTTGGGCTCAGAACTGCAGCTGTGCAGCTGGAACAT 1066  
Db 1286 CAGACAAATAATACCGGTGTTTATTTGGGCAACAGAACTGCAGCTGTGGGCTGGAGCAT 1345  
Qy 1067 TCTGTATTCACTGTCTATTTGTGATGCTCCGGGTGTTTCAACTAGAACTTCAGACCCAA 1126  
Db 1346 TCTGTATTCACTGTCTATTTGTGATGCTCCGGGTGTTTCAACTAGAACTTCAGACCCAA 1405  
Qy 1127 TGTATTGAGAAACTTTAAAGATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTT 1186  
Db 1406 TGTATTGAGAAACTTTAAAGATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTT 1465  
Qy 1187 GTAGCGTAGTCAAGGATCAAGCTCCATCTGTAACCACTCCAGAAAGTTTGTTCAC 1246  
Db 1466 GTAGCGTAGTCAAGGATCAAGCTCCATCCGGAACACCATCCAGAAAGTTTGTTCAC 1525  
Qy 1247 GCATGTCAATCTCATATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCT 1306  
Db 1526 GCATGTCAATCTCATATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCT 1585  
Qy 1307 GCATAAGGATGAAGAGAACAGATGTGTCTATTGTGTTTGGGCACTGCTTGATGAAG 1366  
Db 1586 GCATCAAGGATGAAGAGAACAGATGTGTCTCATCTGTCTGTCTGTCTGTCTGTCTGTCT 1645  
Qy 1367 AAAGTCTTACAGTGTGAGAGCGCTGCAGGAAACAGCTGCACCACTGCATGTCAA 1426  
Db 1646 AGAGCCTGACTGTGTGAAGATGGCTGCAGAAACAGCTGCACCACTGCATGTCCA 1705  
Qy 1427 TTTGGCGAAGAGTGAAGAAATAGAGAACCTTTAATATGTCCCTTTGTAGATCTA 1486  
Db 1706 TCTGGCGAAGAGTGAAGAAATAGAGAACCTTTAATATGTCCCTTTGTAGATCTA 1765  
Qy 1487 AGTGGAGATCTCATGATTTCTACGCCAGATTTGTCAAGTCTGTGAGATTTCCCTCTCTT 1546  
Db 1766 AGTGGAGATCCCATGACTTCTACGCCATGAGTTATCAAGCCCGTGGAGTCCCGGCT 1825  
Qy 1547 CCTCAGAGCTGCACAGCAGCAACCGTACAGCAGCGCTTTGGCTGGATCA---CGAA 1603  
Db 1826 CCTCGAGCTGTCCAGAGCCATCTCTCCCGCAGCAGCCGCTGGCCGAGTACAGCCGA 1885  
Qy 1604 GGAATCAAGAGAGCAATTTAACTTACTTATGAACTCAGCAATTCCTCTCTCTCTCT 1663  
Db 1886 GGAATCAGGAGAGCAATTTAACTTACTTATGAACTCAGCAATTCCTCTCTCTCTCT 1945  
Qy 1664 ACAAGATTTAGCTGAGCAGTGAATTCAGTGTGTTGGAACTGGAATGGAATCTGTTGCTCTTAT 1723  
Db 1946 ACAAGATTTGGCCGAGCCATGGAATTCAGTGTGTTGGAACTGGAATGGAATCTGTTGCTCTTAT 2005

Qy 1724 TTTCTAGAAAATGGAAATGTGAGAGATGGCCCTCAGCGCTCTTTCCCATGATGTCACTG 1783  
Db 2006 TCTCTAGAAACTGGAACTGAAAGAAATGGCCCTTAGCGCTCTTTCCCAAGCGTGTAGTG 2065  
Qy 1784 GGGCCCTGTGTGTGGCAATGGGAGAGCACTGGAAATTTCTGGGGGCGAGCTGGAAGCA 1843  
Db 2066 GGGCCCTGTGTGTGGCAATGGGAGAGCACTGGAAATCTCTGGAGCGCGCAGTGGGGCA 2125  
Qy 1844 GCGCAGTGGGGAGGACCAAGTGGGTCTTCCAGACCAAGTATCTCAGGAGATGTGGTG 1903  
Db 2126 GCTTAAGCGCGGAGCGGCGCAGCGGTCTCTCCAGCCAGCATCTCAGGGGATGTGGTG 2185  
Qy 1904 AGGCATGTGCGAGCTTCTGTCAATGGTCTGTGCTGACCCCTGTCTACAAAGTGTACGTTG 1963  
Db 2186 AGCGTGTCTGAGTCTCTGTCTTAGTCTGCGCTGACCCCTGTCTACAAAGTGTACGTTG 2245  
Qy 1964 CTGCTTTAAAAACATTTAGAGCCATGCTGGTATATATCTCTTCCACAGTGTAGCGGAAA 2023  
Db 2246 CTGCTTTAAAAACATTTAGAGCCATGCTGGTATATATCTCTTCCACAGTGTAGCGGAAA 2305  
Qy 2024 GAATCAAACTTCAGAGACTTCTCCAGCCAGTGTGTAGACCACTCTAGTCAAAATGTGCAAG 2083  
Db 2306 GAATCAAACTTCAGAGACTTCTCCAGCCAGTGTGTAGACCACTCTAGTCAAAATGTGCAAG 2365  
Qy 2084 ATGCCAATAGCCGCAAGTCAAGTGTCCATATCAACACTGTGTGGAACCTGTGCAAGGCC 2143  
Db 2366 ATGCCAAGAGCGGCAAGTCAAGTGTCCATATCTACAGTGTGGAACCTGTGCAAGGCC 2425  
Qy 2144 AAGCAGAGAGTGGCAGTGTGGCAGAGAAATACTAAAGCTGATCTCATTTGTTGTTGTTG 2203  
Db 2426 AAGCAGAGAGTGGCAGTGTGGCAGAGAAATACTAAAGCTGATCTCATTTGTTGTTGTTG 2485  
Qy 2204 GTGTTGATTTATGTTTAAATTTGTTTCTTGGAAACCAAACTGAAATCAAAACAAATTTGCAAG 2263  
Db 2486 GTGTTGATTTATGTTTAAATTTGTTTCTTGGAAACCAAGCTGAAATCAAAACAAATTTGCAAG 2545  
Qy 2264 AACTTCTTGGCGCTTCTCTTATATAGATGAGTGTGTTGGAATTTCTGCTGATTTT 2323  
Db 2546 AACTGTGGGTGCGCTCTCTTATAGACAGTGTGCTGTGGAATTTCTGCTGATTTCT 2605  
Qy 2324 ATCTCATATTTGTCAGTACTGATTTTCAAAAGCTGAGCTGTGTTGAAATCAGATATPAGA 2383  
Db 2606 ATCTCATATTTGTCAGTACTGATTTTCAAAAGCTGAGCTGTGTTGAAATCAGATATPAGA 2665  
Qy 2384 AGCTGTGCTCTTCTTAACTTGTCTTGCAGTCCATTTGATTAATCCCACTCAATGTTG 2443  
Db 2666 AGCTGTCTCTCTTAACTTGTCTTGCAGTCCATTTGCAATTTCCCACTCAATGTTG 2725  
Qy 2444 GCAAACTTTCCAGAGGATCTACTTCAAGTCTGTCAGAGATGGTTACTACAGTACCCCATG 2503  
Db 2726 GCAAGCTCTCTCGAGGATATATCTGAGCTCTGCCAGGATGGTGACCGCAGTCCCGCTG 2785  
Qy 2504 TGTCTTCAAACTGTTAGAAATGCTGAGTGTGTTCCAGTTCCTCACTTCCAGCAGATGC 2563  
Db 2786 TGTCTTCAAACTGTTAGAAATGCTGAGTGTGTTCCAGTTCCTCACTTCCAGCAGATGC 2845  
Qy 2564 GTCCCGTGTGATGGCTATTGTCAGATGAGGTGGAATTTCCGAAAGCCATCCAGTGGCGG 2623  
Db 2846 GCGCGCTCTGATGGCTATTCGCGGATGAGGTAGAAATTTCCGAGGTCACTCCAGTGGTG 2905  
Qy 2624 TAGAAGACATTTGGATGGTCAACAGGACAGCTTCTTGAGGATCTGTGTTCCCAACT 2683  
Db 2906 TGGAGGACATGTGGATGGCATCAGGACAG---CTTACAGGCGGTGGCCCCCAGCAGCT 2962  
Qy 2684 ATCTGGAAACACAGAGAACAGTTCCTGAGTGCACAGTCCATTTAGAGAAATCTGAA 2743  
Db 2963 GTCT-----AGAAACAGCTCTCTTGAGCAGACAGTCCATAGAGAGAAATCTGAA 3013  
Qy 2744 AAGGATTTATGTCTACAAATTTGAGTCCAGTTCAGAGGACATTTCTGAGAGACTGGCCA 2803  
Db 3014 AAGGACTAAGTCTACGAGACTGAGTGCAGCTCGGAGGACATTTCTGACAGACTGGCCG 3073







|      |    |                                                                 |      |
|------|----|-----------------------------------------------------------------|------|
| 1801 | DB | TTCCCTCTTAACTTTGCTTCCATTCCAATCCAAATCCCACTCGATGGTGGCAAGC         | 1860 |
| 2450 | QY | TTTCCAGAAAGATCTACTTGAGTCTTGCAAGAAATGGTTACTACAGTACCCCATGTGTTTT   | 2509 |
| 1861 | DB | TCCTCGGAGGATATATCTGAGCTCTGCCAGGATGGTGACCGCAGTGCCCGCTGTGTTTT     | 1920 |
| 2510 | QY | CAAAATGTTTAGAAATGCTGAGTGTTCAGTTCCTCACTCACATTCACAGGATGCGTCGCC    | 2569 |
| 1921 | DB | CCAAGCTGGTAAACATGCTTAAATGCTTCTGGCTCCACCCCACTTCAACAGGATGCGCGGC   | 1980 |
| 2570 | QY | GTTTGATGGCTATTGCGAGTGAAGTGAATTCGCCGAAGCCATCCAGTTGGCGGTAGAAG     | 2629 |
| 1981 | DB | GTCTGATGGCTATCGCGATGAGTAGAAATTCGCCAGGTTCATCCAGTGGGTGTGGAGG      | 2040 |
| 2630 | QY | ACACTTTGGATGTCACACAGCAGCTTCTTGAGGCATCTGTTCCCAACAACATATCTCG      | 2689 |
| 2041 | DB | ACACTGTGGATGGGCATCAGGACAG---CTTACAGGCGTGGCCCCCGCAGCTGTCT--      | 2095 |
| 2690 | QY | AAACCCAGAGAAACAGTTCCTCGTGAAGTGCACAGTCCATTTAGAGAAAACTGGAAAAAGGAT | 2749 |
| 2096 | DB | -----AGAAAAACAGCTCCCTTGAGCACACAGTCCATAGAGAGAAAACTGAAAAAGGAC     | 2148 |
| 2750 | QY | TATGTGCTACAAATTGAGTGCCAGTTCAGAGACATTTCTGAGAGACTGGCCAGCATTT      | 2809 |
| 2149 | DB | TAAAGTCTCGAGCTGAGTGCCAGCTCGGAGGACATTTCTGACAGCTGGCCGGCTCT        | 2208 |
| 2810 | QY | CAGTAGACCTTCTAGTTCACAAACAAACAAACAAACAGAGCAACCAAGGCCAA           | 2869 |
| 2209 | DB | CTGTAGACTTCCAGCT-----CAACAAACAGAGAAACCAACAAAGCCAG               | 2253 |
| 2870 | QY | TGGTTCAACAAAGAGCAGACCCACAGTCAGTGGTTTGAATCCTCTCTCTTATCTCATC      | 2929 |
| 2254 | DB | CGTTTCAACAAAGAGCAGACCCACAGTCAGTGGTTTGAATCCTCTCTCTTGTGC---TC     | 2310 |
| 2930 | QY | ATTCCCAATTAAATGTTTCAGGCTTGTCACACCCCTCTCTTTCTACCCCATCTGTACCG     | 2989 |
| 2311 | DB | ATGCTCAATTAAATGTTTCCAGACCAATCAACCCCTTGTCTCTCTGCCCCGTCTGTCC---   | 2367 |
| 2990 | QY | CTGCACTGCAACAGATGTTCTTAAGCATAGACTTCAGGATTCATTCCCTGTCAGAAATAC    | 3049 |
| 2368 | DB | -----CAGATTTCTTAGCACAGACCCAGGCAATTTGTTCCCTGCAAAATAC             | 2415 |
| 3050 | QY | CTTCTGCACTCTCTCAACACAGGCGAAGTTTCTCTTCAATTTCCACAGAAATGTCTCTG     | 3109 |
| 2416 | DB | CTTCCGATCTCTCAGACACAGCGCAAGTCTCTCTCAATTTCCAGAGAACTGTCTGT        | 2475 |
| 3110 | QY | AAAAAAGACTCAGATAAACTTTCCCGAGTCTTTACTCAGTCAAGACCCCTGCCCTCCA      | 3169 |
| 2476 | DB | AACACCGAGACTCAGACCACTCTCCCGAGTCTTCACTCAGTCAAGACCCCACTCCA        | 2535 |
| 3170 | QY | GTAACATACACAGGCGAAAGCATCTAGACTACCCAGTAAATACAGTAAACAGGGAG        | 3229 |
| 2536 | DB | GTAACATACACAGGCGAAAGCCATCCCGACCCGTTCCGGCAGTACAAAGCAACTAGGGG     | 2595 |
| 3230 | QY | ATCCCTCAAAAAATAGCATGACATTTGATCTGAACAGTAGTTCCAAATGTGATGACAGCT    | 3289 |
| 2596 | DB | ACGCCACAAAAATAGCATGACATTTGATCTGGCAGTGTCTTCAGGTGTGACGACAGCT      | 2655 |
| 3290 | QY | TTGGCTGACGACGAATAGTAGTAATGCTGTTATACCCAGTGACGAGAGAGTGTCAACC      | 3349 |
| 2656 | DB | TTGGCGCGCGGCGCAACAGTGGCAACCGCGTCAACCCAGCGACGACAGTGTTCACGC       | 2715 |
| 3350 | QY | CAGTAGAGGAGAAATGACAGATTAGATGTCAATACAGAGCTCAACTCCAGTATTGAGGACC   | 3409 |
| 2716 | DB | CGGTGGAGGACAAGTGCAGGTTAGATGTGAACACCGAGCTCACTCCAGCATCGAGACC      | 2775 |
| 3410 | QY | TTCTTTGAAGCATCTATGGCTTCAAGTGATACACAGTAACTTTTAACTCAGAAGTTGCTG    | 3469 |
| 2776 | DB | TTCTTTGAAGCATCTATGGCTTCAAGTGACACGACGATCACTTTCAAGTCCGAAGTGGCG    | 2835 |
| 3470 | QY | TCCTGTCTCTGTAAAAAGGCTGAAAAATGATGATACCTACAAAGATGATGTGAATCAATAC   | 3529 |

|    |      |                                                                     |      |
|----|------|---------------------------------------------------------------------|------|
| Db | 2836 | TCCTCTCTCTCGGAAAAAGCCGAAAAATGACGACACCTTCAAAAGACGAGCTCAATCATTAATC    | 2899 |
| Qy | 3530 | AAAAGTGCAAAGAGAGATGGAAGCTGAAAGAAAGAAAGCTTTTAGCAATTTGCCATGGCAA       | 3589 |
| Db | 2896 | AAAAGTGCAAAGAAAAAGATGGAAGCTGAAAGAGAGAGAGGCTTTTAGCGATGCCATGGCGA      | 2955 |
| Qy | 3590 | TGTCAGCGTCTCAGGATGCCCTCCCATAGTTTCCCTCAGCTGCAGGTTGAAAAATGGAGAAG      | 3649 |
| Db | 2956 | TGTCAGCGTCTCAGGATGCCCTCCCATCGTCCCTCAGCTGCAGGTTGGAATAATGGAGAG        | 3015 |
| Qy | 3650 | ATATCATCATTTATTCACAGGATACACAGAGACTCTTACAGACATACACAAAGCAAAAC         | 3709 |
| Db | 3016 | ATATATCATCATTCAGCAGGACACACCAGAAACTCTTCAGGACATACACAAAGCGGAAC         | 3075 |
| Qy | 3710 | AACCGTATAGAGAAGACACTGAATGCTGAAAGGTCAAACAGATAGGCTTTGGAGCATTTT        | 3769 |
| Db | 3076 | AGCCTTCACAGAAAGACGCTAGTGGCTGNAAGCCAGCAGATAGGCTCGAGCATTTT            | 3135 |
| Qy | 3770 | CTTCTTTGTTATCAGGCTCAAGATGTGGGAACCTGGAACTTTAATAGCTGTAAACACAGTGA      | 3829 |
| Db | 3136 | CTTCTTTGTTATCAGGCTCAAGATGTGGAACTGGAACTTTAATAGCTGTAAACACAGTGA        | 3195 |
| Qy | 3830 | CTTATGTCAGAAACACATCTTCTGAGCAAGAAAGTAGTAGAAGCACTTAAGAGAAAGAGA        | 3889 |
| Db | 3196 | CTTATGTCAGAAACACATCTTCTGAGCAAGAAAGTAGTAGAAGCACTTAAGAGAAAGAGA        | 3255 |
| Qy | 3890 | TAAGAATGATGAGCCATCTGAATCATCTCCAAACATCAATTAGGATTTGGGAGCCACGTGTG      | 3949 |
| Db | 3256 | TAAGAATGATGAGCCATCTGAATCATCTCCAAACATCAATTAGGATTTGGGAGCCACGTGTG      | 3315 |
| Qy | 3950 | AGAAGAGCAATTACAATCTCTTCATTGAATGGAATGGCAGGGGATCGTGCGTCAATTGTC        | 4009 |
| Db | 3316 | AGAAGAGCAATTACAATCTCTTCATTGAATGGAATGGCAGGGGATCGTGCGTCAATTGTC        | 3375 |
| Qy | 4010 | TGAGTAAATATGAGGCTTCAAGAAATCAGTAGTTATTAACCTACATGAAACAGTTACTCC        | 4069 |
| Db | 3376 | TGAGTAAATATGAGGCTTCAAGAAATCAGTAGTTATTAACCTACATGAAACAGTTACTCC        | 3435 |
| Qy | 4070 | GTGCGCTTTTCGTATCTCCATGAGAAACCAAATCAATTCACAGAGATGTCAAAGGTGCCAATT     | 4129 |
| Db | 3436 | GTGCGCTTTTCGTATCTCCATGAGAAACCAAATCAATTCACAGAGATGTCAAAGGTGCCAATT     | 3495 |
| Qy | 4130 | TGCTAAATGTGACGACTGTGCAGAGACTAAGAAATTCAGAAATTTTGGAGCTTGCAGCCAGGT     | 4189 |
| Db | 3496 | TGCTCAATGTGACGACGACGCGTGCAGAGGCTGAGAAATTCAGAAATTTTGGAGCTTGCAGCCAGGT | 3555 |
| Qy | 4190 | TGCGATCABAAGGAACGTGTGCGAGGAGGTTTCAGGGACAAATTAAGTTCGGGACAAATTCGAT    | 4249 |
| Db | 3556 | TGCGATCABAAGGAACGTGTGCGAGGAGGTTTCAGGGACAAATTAAGTTCGGGACAAATTCGAT    | 3615 |
| Qy | 4250 | TTATGGCACTGAGGTAATAAGAGGTCACAGTATGGAAGAGGCTGTGATGTATGGAGTG          | 4309 |
| Db | 3616 | TCATGGCGCTCAGGTCCTTAAGAGGTCAGCAGATATGTTAGGAGGCTGTGATGTATGGAGTG      | 3675 |
| Qy | 4310 | TTGCGTGTGCTATTATAGAAATGCGTTGTCAAAAACCAACATGCAATTCAGAGAAAAACACT      | 4369 |
| Db | 3676 | TTGCGTGTGCTATTATAGAAATGCGTTGTCAAAAACCAACATGCAATTCAGAGAAAAACACT      | 3735 |
| Qy | 4370 | CCAATCATCTTGCTTTTGATATTTAAGATTCCTAGTGCAACTACTGCTCCATTCGATTCGCTT     | 4429 |
| Db | 3736 | CCAATCATCTTGCTTTTGATATTTAAGATTCCTAGTGCAACTACTGCTCCATTCGATTCGCTT     | 3795 |
| Qy | 4430 | CACATTTGCTCTCGTGGTTTACAGAGATGTGCTCTTCGTTGTTTAGAACTTCAACCTCAGG       | 4489 |
| Db | 3796 | CACACCTGTCCCTCGTGGTTTACAGAGATGTGCTCTTCGTTGTTTAGAACTTCAACCTCAGG      | 3855 |
| Qy | 4490 | ACGACCTCCATCAAGAGACTACTGAAGCATCCAGTCTTTTCGTAATCGATGAGTAG            | 4545 |
| Db | 3856 | ACCGGCTCTCGTCAAGAGACTGTCTGAAACATTCGGTCTTCGTAATCAACGTTGTTAG          | 3911 |





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APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIORITY INFORMATION:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr. Esq.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: CPI-004DVCP2
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3260 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MEKK
STRAIN: murine
IMMEDIATE SOURCE:
LIBRARY: mouse liver
CLONE: MEKK cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..485
NAME/KEY: CDS
LOCATION: 486..2501
NAME/KEY: 3'UTR
LOCATION: 2502..3260
US-08-472-934-1

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Query Match      37.3%; Score 1955.6; DB 1; Length 3260;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

QY 1996 TATACCTCTTGCACAGTTTAGCGGAAAGAAATCAAACTTCAGAGACTTCTCCAGCGCAGTT 2055
Db 1 TACACTCTTGCACAGTTAGCGGAAAGAAATCAAACTTCAGAGACTTCTCCAGCGCAGTT 60

QY 2056 GTAGACACATCTCTAGTCAAAATGTGCAGATGCCAATAGCGGCAAGTCAGTGTCCATA 2115
Db 61 GTAGACATCTCTCTCAAGTGTGCAGAT-CCAAACAGCGCGCAGAGTCAGTGTCCATA 119

QY 2116 TCAACACTGTGTGAATGTGCAAGGCCCAAGCAGAGAGTTCGCGAGTTGGCAGAGAAATA 2175
Db 120 TCTACAGTCTGTGAATCTGTGCAAGGCCCAAGCAGAGAGTTCGCGAGTTGGGAGAAATA 179

QY 2176 CTAAAGCTGGATGCCAATGGTATGGTGTGTGATTAATGTCTTAAATGTATTCTTGGGA 2235
Db 180 CTAAAGCTGGTGTCCATCGGGTGGTGTGTGATTAATGTCTTAAATGTATTCTTGGGA 239

QY 2236 AACCAAACTGAATCAAACTGGCAAGAACTTCTTGGCGGCTTGTCTTATAGATAGA 2295
Db 240 AACCAAGCTGAATCAAACTGGCAAGAACTTCTTGGCGGCTTGTCTTATAGACAGG 299

QY 2296 CTGTCTTGGAAATTCCTCTGAATTTTATCTCATATTGTGCACTGATGTTTCAAA 2355
Db 300 TTGCTGTGGAAATTCCTCTGAATTTTATCTCATATTGTGCACTGATGTTTCAAA 359

QY 2356 GCTGACGCTGTGAATCAGGTATAGAGCTGTCTCTTAACTTGTCTTAACTTGTCTTGA 2415
Db 360 GCTGACGCTGTGAATCAGGTATAGAGCTGTCTCTTAACTTGTCTTAACTTGTCTTGA 419

QY 2416 TCCATTGATAATTCACACTCAATGGTGTGGCAAACTTTCCAGAGAGATCTACTTGTAGTTCT 2475
Db 420 TCCATTGATAATTCACACTCAATGGTGTGGCAAGCTCTCTCGGAGGATATATCTGAGCTCT 479

QY 2476 GCAAGATGGTACTACAGTACCCCATGTGTTTTCAAACTGTAGAAATGCTGAGTGT 2535

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Db 480 GCCAGGATGGTGACCGGAGTGCCTGCTGTTTTTCCAAAGCTGGTAACCATGCTTAATGCT 539
QY 2536 TCCAGTTCCACTCACTTCCACAGGATCGTGCCTGTTTGGTGGCTATTGGAGATGAGTG 2595
Db 540 TCTGGCTCCACCCACTTCCACAGGATCGCGGGCTGTGTGCTGCTGCGGATGAGGTA 599
QY 2596 GAAATTCGGAAGCCATCCAGTTGGGCTGAGAAGACACTTTGGATGTCTAACAGGACAGC 2655
Db 600 GAAATTCGGAAGCTCATCCAGTGGTGTGAGGACACTGTGGATGGCATCAGGACAG- 658
QY 2656 TTCTTGGAGGACATCTGTTCCCAAACTATCTTGGAAACCAACAGAGACAGTTCCTCTGAG 2715
Db 659 --CTTACAGCCGTGGCCCCCACCAGCTGTCT-----AGAAAACAGCTCCCTTGGAG 707
QY 2716 TGCAAGTCCATTTAGAGAAAACTGGAAAAGGATTAATGTCTCAAAATTTGAGTGCACGT 2775
Db 708 CACACAGTCCATAGAGAGAAACTGGAAAAGGACTTAAGTGTCTACGAGACTGAGTGCCAGC 767
QY 2776 TCAGAGGACATTTCTGAGAGACTGGCCAGCATTTTCAGTAGACCTTCTAGTTCAACAACA 2835
Db 768 TCGAGGAGACATTTCTGACAGCTGGCCGGCTCTCTGTAGGACTTCCCACT----- 819
QY 2836 ACAACAAACAAACAACAGAGCAACCAAGGCCAATGTTTCAAAACAAAGGACAGACCCAC 2895
Db 820 -----CAACAAACAACAGAGCAACCAAGGCCAGCGGTTCAACAAAGGACAGACCCAC 872
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QY 2956 TCAACCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3015
Db 930 TCAGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 974
QY 3016 CATGACTTCAGGATTCATTTCCCTGCGAATTAACCTTCTGCTCTCTCTCTCTCTCTCTCT 3075
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QY 3136 CCAGTCTTTACTCAGTCAAGACCTTGTCCCTCTCAGTAAACATACAGGCGCAAGGCACT 3195
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QY 3496 GATGATACCTTACAAAGATGATGTAATCATAAATCAAAAGTCAAAAGAGAGATGGAAGCT 3555
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QY 3556 GAAGAAGAGAGCTTTAGCAATTTGCCATTTGCGAATGTGACGCTCTCAGGATGCTCTCTCT 3615

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1515 GAAGAGGAGGAGGCTTTAGCGATCCCATGGCGATGTGTCAGGATGCCCTCCCC 1574  
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3976 GAATGATCGCAGGGGATCGGTGCTCATTTGCTGAGTAATATGAGGCTTCAAGAA 4035  
1935 GAGTGTGATGGCGGAGGATCTGTGGCTCACCTCTTGAATTAATACGGAGCTTCAAGGAG 1994  
4036 TCAGTAGTTATTAATCTACACTGAAAGTTACTCCGTGGCTTTCGTATCTCATGAAAC 4095  
1995 TCAGTGTGATTAATCTACACTGAAAGTTACTCCGTGGCTTTCGTATCTCATGAAAC 2054  
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2055 CAGATCATTTACAGAGACGTCAAAGTGCCAAATTTGCTTAATGACAGCACTGGTCAGAGA 2114  
4156 CTGAAGTTGTCAGATTTGGAGCTGAGCGGCTGGCATCAAAAGGACTGGTCAGAGA 4215  
2115 CTGAAGTTGTCAGATTTGGAGCTGAGCGGCTGGCATCAAAAGGACTGGTCAGAGA 2174  
4216 GAGTTTCAGGAGCAATTAATGCGGCAATTTGATGTTATGCGACCTGAGGTACTAAGAGT 4275  
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4516 AAGCATCCAGTCTTCTGTTTGTAGAACTTCAACCTCAGAGCAGACCTCCATCAAGAGAG 4575  
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2595 CCCTCAGCCACTGAACAGGCGCAGTGGGAAACCTTCACTCAAGTATGTG 2653

QY 4692 ATTGCAAAATCATGATCTCTTACCTAAGCTCAGTATGCA-AAAGCCCAAACTAGTGCAGAA 4750  
Db 2654 ATTGCAAAATCATGATCTCTTACCTAAGCTCAGTATGCAACATCTTACAGCTCGTGCAGAA 2713  
QY 4751 ACTGTAACCTGTCCTTTCAAGAACTGGCCCTAGTGAACAGGAAACAAATGAAGTTTG 4810  
Db 2714 ACTGCACACGTCCTTTTCAAGAACTGGCCCTAGTGAACAGGAAACAAATGAAGTTTG 2773  
QY 4811 CATGACTAAATTCAGAAACATAATTTATTTTGGAGCACTTTTTCAGCAA 4864  
Db 2774 CATGACTAAAGAACAGACATTAATTTA-TTTTGGAGCACTTTTTCAGCTA 2825

## RESULT 7

US-08-323-460A-1  
; Sequence 1, Application US/08323460A  
; Patent No. 5854043  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, GARY L.  
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL  
; TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH  
; STREET: 1700 LINCOLN STREET, SUITE 3500  
; CITY: DENVER  
; STATE: CO  
; COUNTRY: USA  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/323,460A  
; FILING DATE: 14-OCT-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER: US 08/049,254  
; FILING DATE: 14-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOVARIK, JOSEPH E.  
; REGISTRATION NUMBER: 33,005  
; REFERENCE/DOCKET NUMBER: 2879-1-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 303/863-9700  
; TELEFAX: 303/863-0223  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3260 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEetical: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: MEKK  
; STRAIN: murine  
; IMMEDIATE SOURCE:  
; LIBRARY: mouse liver  
; CLONE: MEKK cDNA  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: 1..485  
; NAME/KEY: CDS  
; LOCATION: 486..2501  
; NAME/KEY: 3'UTR  
; LOCATION: 2502..3260  
; US-08-323-460A-1

|                                                                                                                                |      |                                                                 |      |     |      |     |        |      |            |
|--------------------------------------------------------------------------------------------------------------------------------|------|-----------------------------------------------------------------|------|-----|------|-----|--------|------|------------|
| Query Match 37.3%; Score 1955.6; DB 2; Length 3260;<br>Best Local Similarity 82.7%; Pred. No. 0;<br>Matches 2376; Conservative |      |                                                                 |      |     |      |     |        |      |            |
| QY                                                                                                                             | 1996 | TATACCTCTGCGACAGTTTAGGGGAAAGAAATCAAACTTCAGAGACTTCTCCAGCCAGTT    | 2055 | 10; | Gaps | 54; | Indels | 444; | Mismatches |
| DB                                                                                                                             | 1    | TACACTCCCTTGGCCACAGTCTGGCAGAAAGAAATCAAACTTCAGAGACTTCTCCGGCCAGTT | 60   |     |      |     |        |      |            |
| QY                                                                                                                             | 2056 | GTAGACACCATCTCTAGTCAAAATGTGCAGATGCCAATAGCCGACAAAGTCAGTGTCCCAT   | 2115 |     |      |     |        |      |            |
| DB                                                                                                                             | 61   | GTAGACACTATCTCTGCAAGTGTGCAGAT-CCACAGCCGACGAGTCAGTGTCCCAT        | 119  |     |      |     |        |      |            |
| QY                                                                                                                             | 2116 | TCMAACTGTGTGAACTGTGCAAGCCCAAGCAGAGAGTTGGCAGTTGGCAGAGAAATA       | 2175 |     |      |     |        |      |            |
| DB                                                                                                                             | 120  | TCTACAGTGTGGAATCTGCAAGGCCCAAGCAGAGAGTGGCGTTGGGAGAGAAATA         | 179  |     |      |     |        |      |            |
| QY                                                                                                                             | 2176 | CTAAAAGCTGGATTCATTTGATTTGGTGTGTTGATTATGTTCTTAAATGTTATCTTGA      | 2235 |     |      |     |        |      |            |
| DB                                                                                                                             | 180  | CTTAAAGCTGGTCCATCGGGTTGGTGTGTCGATTACGTCTTAAGTTGTAATCTTGA        | 239  |     |      |     |        |      |            |
| QY                                                                                                                             | 2236 | AACCAACTGAATCAAACTAATGGCAAGAACTTTTGGCGGCTTTGTCTTATAGATAGA       | 2295 |     |      |     |        |      |            |
| DB                                                                                                                             | 240  | AACCAAGCTGAATCAAACTAATGGCAAGAACTTTTGGCGGCTTTGTCTTATAGACAG       | 299  |     |      |     |        |      |            |
| QY                                                                                                                             | 2296 | CTGTTGTGGAATTTCTGCTGGAATTTTATCCTCATATGTGAGTACTGATGTTTCAAA       | 2355 |     |      |     |        |      |            |
| DB                                                                                                                             | 300  | TTGCTGTGGAATTTCTGCTGGAATTTCTATCCTTCATATTTGTGATGTCATGTCACMA      | 359  |     |      |     |        |      |            |
| QY                                                                                                                             | 2356 | GCTGAGCTGTTGAAATTCAGGTATAAGAGCTGCTCTCCTCTTAACTTTCTTTGAC         | 2415 |     |      |     |        |      |            |
| DB                                                                                                                             | 360  | GCTGAGCTGTTGAAATTCAGGTATAAGAGCTGCTCTCCTCTTAACTTTCTTTGCAA        | 419  |     |      |     |        |      |            |
| QY                                                                                                                             | 2416 | TCCATTGATTAATTCACACTCAATGTTGGCAACTTTCCAGAGGATCTACTGTGTTCT       | 2475 |     |      |     |        |      |            |
| DB                                                                                                                             | 420  | TCCATTGATTAATTCACACTCAATGTTGGCAACTTTCTCGAGGATATATCTGAGCT        | 479  |     |      |     |        |      |            |
| QY                                                                                                                             | 2476 | GCAAGATGTTTACTACAGTACCCCATGTTGTTTCAAACTGTTGAAATGTTGAGTGT        | 2535 |     |      |     |        |      |            |
| DB                                                                                                                             | 480  | GCCAGGATGTGACCGCAGTGCCCGCTGTGTTTCCAGCTGTTAACCATGTTAATGCT        | 539  |     |      |     |        |      |            |
| QY                                                                                                                             | 2536 | TCAGTTCCTACTCATCTCAGAGATGCGTGGCGGTTGATGCTATTCAGATGAGGTG         | 2595 |     |      |     |        |      |            |
| DB                                                                                                                             | 540  | TCTGGCTCCACCCACTTCACAGGATGCGCGCGCTGTGATGCTATCGCGGATGAGTA        | 599  |     |      |     |        |      |            |
| QY                                                                                                                             | 2596 | GAAATTCGGAAGCCATCCAGTTGGCGTGAAGACACTTTGATGTTCAACAGACAGC         | 2655 |     |      |     |        |      |            |
| DB                                                                                                                             | 600  | GAAATTCGCGAGTCTACAGCTGGGTGTGAGGACACTGTGATGGCATCAGGACAG          | 658  |     |      |     |        |      |            |
| QY                                                                                                                             | 2656 | TTCTTGAGGCATCTGTTCCTCAACACTATCTGGAAACCAACAGAACAGTTCCCTGAG       | 2715 |     |      |     |        |      |            |
| DB                                                                                                                             | 659  | --CTTACAGCCGTTGGCCCGCCACAGCTGTCT-----AGAAACACAGCTCCCTTGAG       | 707  |     |      |     |        |      |            |
| QY                                                                                                                             | 2716 | TGCACAGTCCATTTAGAGAAACTGGAAAGGATTTAGTCTACAAATTTAGTGCAGT         | 2775 |     |      |     |        |      |            |
| DB                                                                                                                             | 708  | CACACAGTCCATAGAGAGAAACTGGAAAGGATTTAGTCTACAGACTAGTGGCAGC         | 767  |     |      |     |        |      |            |
| QY                                                                                                                             | 2776 | TCAGAGACATTTCTGAGAGACTGGCCAGCATTTAGTAGGACCTTCTAGTTCAACAACA      | 2835 |     |      |     |        |      |            |
| DB                                                                                                                             | 768  | TCGAGGACATTTCTGACAGACTGGCCGCGTCTCTGTAGGACTTCCAGCT-----819       |      |     |      |     |        |      |            |
| QY                                                                                                                             | 2836 | ACAACACACACACAGAGCACCAAGCCATGTTCTCAACAAAGGACAGCCCCAC            | 2895 |     |      |     |        |      |            |
| DB                                                                                                                             | 820  | -----CACACACACAGACCAACCAAGCCGCGTTCAACAAAGGACAGCCCCAC            | 872  |     |      |     |        |      |            |
| QY                                                                                                                             | 2896 | AGTCAGTGTGAACTCTCTCTCTTTATCTCATCATTTCCAAATTAATTTCCAGCCTTG       | 2955 |     |      |     |        |      |            |
| DB                                                                                                                             | 873  | AGTCAGTGTGAACTCTCTCTCTTTGTC--TCATGCTCAATTAATTTCCAGCAGCA         | 929  |     |      |     |        |      |            |
| QY                                                                                                                             | 2956 | TCACCCCTCTCTCTTACCCCATCTGTACCAGCTGGCAACAGATGTTCTTAAG            | 3015 |     |      |     |        |      |            |
| DB                                                                                                                             | 930  | TCAGCCCTCTCTCTCTGCCCCGCTCTGTC-----CAGATATTTCTAAG                | 974  |     |      |     |        |      |            |
| QY                                                                                                                             | 3016 | CATAGACTTCAGGATTCATTTCCCTGCGAATACTTCTGCACTCTCTCAACACAGCGC       | 3075 |     |      |     |        |      |            |
| DB                                                                                                                             | 975  | CACAGACCCAGGCAATTTGTTCCCTGCAAAATACCTTCCGCACTCTCTCAGACACAGCGC    | 1034 |     |      |     |        |      |            |
| QY                                                                                                                             | 3076 | AAGTTTTCTCTCAATTTCCACAGAAAGTGTCTTGAAACAAAGACTCAGATAAATTTCC      | 3135 |     |      |     |        |      |            |
| DB                                                                                                                             | 1035 | AAGTTCTCTCTCAATTTCCAGAGAACTGTCTTGAAACCGAGACTCAGACAGCTCTCC       | 1094 |     |      |     |        |      |            |
| QY                                                                                                                             | 3136 | CCAGTCTTTTACTCAGTCAAGACCTTTGCCCTCCAGTAAACATACACAGGCGCAAGCCATCT  | 3195 |     |      |     |        |      |            |
| DB                                                                                                                             | 1095 | CCAGTCTTTTACTCAGTCAAGACCCCTCCAGTAAACATACACAGGCGCAAGCCATCT       | 1154 |     |      |     |        |      |            |
| QY                                                                                                                             | 3196 | AGACTTACCCAGGTAAATCAAGTAAACAGGAGATCCCTCAAAATATAGATGACACTT       | 3255 |     |      |     |        |      |            |
| DB                                                                                                                             | 1155 | CGACCCCTTCCGGCAGTACAAGCAAACTAGGGGACCCACAAAGTATGATGACACTT        | 1214 |     |      |     |        |      |            |
| QY                                                                                                                             | 3256 | GATCTGAACAGTATGTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCAATATGATTAAT   | 3315 |     |      |     |        |      |            |
| DB                                                                                                                             | 1215 | GATCTGGCAGTGTCTCCAGTGTGACGACAGCTTTGGCGCGCGGCAACAGTGGCAAC        | 1274 |     |      |     |        |      |            |
| QY                                                                                                                             | 3316 | GCTGTTATACCCAGTACGAGACAGTGTTCACCCAGTAGAGGAGAAATCGAGATGAT        | 3375 |     |      |     |        |      |            |
| DB                                                                                                                             | 1275 | GCGCTCATACCCAGCAGCAGAGAGTGTTCACGCCGTGGAGGACAAAGTGCAGTTAGAT      | 1334 |     |      |     |        |      |            |
| QY                                                                                                                             | 3376 | GTCAATACAGAGCTCAACTCCAGTATTSAGGACCTTTTGAAGCATCTATGCCCTTCAAGT    | 3435 |     |      |     |        |      |            |
| DB                                                                                                                             | 1335 | GTGAACCCAGCTCAACTCCAGCATCGAGGACCTTTTGAAGCATCCATGCTTCAAGT        | 1394 |     |      |     |        |      |            |
| QY                                                                                                                             | 3436 | GATCAACAGTAACTTTTAACTGAGAAGTGTCTGCTGCTCTCTGAAAAGGCTGAAAT        | 3495 |     |      |     |        |      |            |
| DB                                                                                                                             | 1395 | GACACGACAGTCACTTTTCAAGTCCGAAGTCCCGTCTCTCTCGGAAAAGGCGCAAAAT      | 1454 |     |      |     |        |      |            |
| QY                                                                                                                             | 3496 | GATGATACCTCAAAAGATGATGTAATCAATAATCAAAAGTGCAAAGAGAGATGGAAGCT     | 3555 |     |      |     |        |      |            |
| DB                                                                                                                             | 1455 | GACGACCTTCAAAAGACGCTCAATCATATCAAAAGTGCAAAGAGAGATGGAAGCT         | 1514 |     |      |     |        |      |            |
| QY                                                                                                                             | 3556 | GAAAGAGAGAGCTTTTAACTAGCAATGTCGCAATGTGAGGCTCTCAGGATGCCCTCCC      | 3615 |     |      |     |        |      |            |
| DB                                                                                                                             | 1515 | GAAAGAGAGAGGCTTTTAACTAGCAATGTCGCAATGTGAGGCTCTCAGGATGCCCTCCC     | 1574 |     |      |     |        |      |            |
| QY                                                                                                                             | 3616 | ATAGTCTCTCAGCTGAGGTTTGAATGGAAGATATCATCATTTTCAACAGGATACA         | 3675 |     |      |     |        |      |            |
| DB                                                                                                                             | 1575 | ATGTTCTCTCAGCTGAGGTTTGAATGGAAGATATCATCATTTTCAACAGGATACA         | 1634 |     |      |     |        |      |            |
| QY                                                                                                                             | 3676 | CCAGAGCTTACACAGGACATACCAAGCAAAACCAACCGTATAGAGAGACACTGAATGG      | 3735 |     |      |     |        |      |            |
| DB                                                                                                                             | 1635 | CCAGAGCTTACACAGGACATACCAAGCAAAACCAACCGTATAGAGAGACACTGAATGG      | 1694 |     |      |     |        |      |            |
| QY                                                                                                                             | 3736 | CTGAAGCTCAACAGTACGCTTTGAGCAATTTCTTCTGTTATCAGGCTCAAGATGTG        | 3795 |     |      |     |        |      |            |
| DB                                                                                                                             | 1695 | CTGAAGCTCAACAGTACGCTTTGAGCAATTTCTTCTGTTATCAGGCTCAAGATGTG        | 1754 |     |      |     |        |      |            |
| QY                                                                                                                             | 3796 | GGAACTGGAACTTTAATGGCTGTAAACAGGTGACTTATGTCAGAAACACATCTTCTGAG     | 3855 |     |      |     |        |      |            |
| DB                                                                                                                             | 1755 | GGAACTGGAACTTTAATGGCTGTAAACAGGTGACTTATGTCAGAAACACATCTTCTGAG     | 1814 |     |      |     |        |      |            |
| QY                                                                                                                             | 3856 | CAAGAGAGTATGATAGAGCACTAAGAGAGAGATAGAAATGATGAGCCATCTCAATCAT      | 3915 |     |      |     |        |      |            |
| DB                                                                                                                             | 1815 | CAGGAGAGGTTGTTGAAGCTTTGAGGAAAGAGATCCGATGATGGGTCACTCAACCAT       | 1874 |     |      |     |        |      |            |
| QY                                                                                                                             | 3916 | CCAAACATCATTTAGGATTTGGGAGCCACAGTGTGAGAGAGCAATTTACAATCTTCTTCAAT  | 3975 |     |      |     |        |      |            |
| DB                                                                                                                             | 1875 | CCAAACATCATTTAGGATTTGGGAGCCACAGTGTGAGAGAGCAATTTACAATCTTCTTCAAT  | 1934 |     |      |     |        |      |            |
| QY                                                                                                                             | 3976 | GAATGATGGCAGGGGATCGTGGCTCATTTGCTGATTAATATGAGGCTTCCAAAGAA        | 4035 |     |      |     |        |      |            |
| DB                                                                                                                             | 1935 | GATGATGGGCGGAGGATCTGTGGCTCACCTCTTGAAGTAAATACGGAGCTTTCAAGAG      | 1994 |     |      |     |        |      |            |
| QY                                                                                                                             | 4036 | TCAGTATGTTTAACTACACTGAACAGTGTACTCCGTGGCTTTTCTGATCTCCATGAAAC     | 4095 |     |      |     |        |      |            |
| DB                                                                                                                             | 1995 | TCAGTCTGTCATTAATCACTGAGCAGTTACTGCGTGGCTTTTCTATCTCTCCAGAGAC      | 2054 |     |      |     |        |      |            |
| QY                                                                                                                             | 4096 | CAAAATCATTCAGAGATGTCAAAGGTGCCAATTTGCTTAATGTACAGCACTGGTCAGAGA    | 4155 |     |      |     |        |      |            |







QY 4516 AAGATCCAGTCTTTGCTACTACATGCTAGCAATATGCGATCAACTCAGTAGAAAC 4575  
DB 2475 AAACATCCGCTCTTCGCTACCACTGCTAGTAAATTTTCAGATCAGCTCTAATGAGAC 2534  
QY 4576 AGATGCTCAACAAGAGAAAAAATCTG- - - - TGGGAAACCAATGATATTTCTACTGG 4631  
DB 2535 AGGATATCGAACCGGAGAGAGAAAGAACTTGTGGCGCACCATGCGCTAACCGCAG 2594  
QY 4632 CCATGATGCACTGAACAGCTATGAACGAGGCGCAGTGGGAAACCCCTTACCTAAGTATGTG 4691  
DB 2595 CCTCAGCCATCTGAACAGCAGAAACCGGGCCAGCGGGAA- CCGTACCTAAGCATGTG 2653  
QY 4692 ATTGACAAATCATGATCTCTAAGCTAGCTAGTATGCA- AAGCCCAAACTAGTGCAGAA 4750  
DB 2654 ATTGACAAATCATGACCTGCTAAGCTAGCTAGTATGCA- AAGCCCAAACTAGTGCAGAA 2713  
QY 4751 ACTGTAACCTGCTCTTCAAGAACTGCGCTAGTGAACAGGAAACAAATGAAGTTTG 4810  
DB 2714 ACTGACACCGTGGCTTTCAGAGGACTGGCTCTGGGACACGAGGAGGATGGGTTTG 2773  
QY 4811 CATGACTAAATGCAAGACATAATTTTATTTTGGAGCACTTTTTCAGCAA 4864  
DB 2774 CATGACTAAAGAACAGACATAAATTTA- - - - TTTTGGAGCACTTTTTCAGCTA 2825

## RESULT 9

US-08-461-145C-1  
; Sequence 1, Application US/08461145C  
; Patent No. 6074861  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, GARY L.  
; TITLE OF INVENTION: NOVEL MEKK PROTEINS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lahive and Cockfield, LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,145C  
; FILING DATE: 5-JUNE-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/049,254  
; FILING DATE: 11-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/323,460  
; FILING DATE: 14-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/11690  
; FILING DATE: 14-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/04178  
; FILING DATE: 15-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/354,516  
; FILING DATE: 21-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kara, Catherine J.  
; REGISTRATION NUMBER: P-41,106  
; REFERENCE/DOCKET NUMBER: CPI-004CN1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 1:

## SEQUENCE CHARACTERISTICS:

LENGTH: 3260 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MEKK  
STRAIN: murine  
IMMEDIATE SOURCE:  
LIBRARY: mouse liver  
CLONE: MEKK cDNA  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..485  
NAME/KEY: CDS  
LOCATION: 486..2501  
NAME/KEY: 3'UTR  
LOCATION: 2502..3260

US-08-461-145C-1

## Query Match

37.3%; Score 1955.6; DB 3; Length 3260;

Best Local Similarity 82.7%; Pred. No. 0;

Matches 2376; Conservative 0; Mismatches 444; Indels 54; Gaps 10;

QY 1996 TATACTCTTGGCCACAGTTTAGCGGAAGAAATCAAACTTCAGAGACTTCTCCAGCCAGTT 2055  
DB 1 TACACTCTTGGCCACAGTTAGCGGAAGAAATCAAACTTCAGAGACTTCTCCAGCCAGTT 60  
QY 2056 GTAGACACCATCTCTAGTCAAAATGTGCAGATGCCAATAGCCGCAAGTCAAGTGTCCATA 2115  
DB 61 GTAGACACTATCTCTGCAAGTGTGCAGAT-CCACAGCGCCAGAGTCAAGTGTCCATA 119  
QY 2116 TCAACACTGTGGAACCTGTGCAAGCCGACAGAGAGTTCGCAGTTCGCGAGAAATA 2175  
DB 120 TCTACAGTGTGGAACCTGTGCAAGCGGCAAGCAGGAGAGTTCGCGTTCGCGAGAAATA 179  
QY 2176 CTAAAGCTGGATCCCATTTGGTATTGGTGGTGTGATTGTCTTAAATTTGATTCTTGA 2235  
DB 180 CTTAAGCTGGTCCATCGGGTGTGTTGTTGTTGATTGTTTAAAGTTGATCTCTGA 239  
QY 2236 AACCAACTGAATCAAACTTGGCAAGAACTTCTTGGCGGCTTTGCTCTTATAGATA 2295  
DB 240 AACCAAGCTGAATCAAACTTGGCAAGAACTTCTTGGCGGCTTTGCTCTTATAGACAG 239  
QY 2296 CTGTTGTTGGAATTTCTCTGCTGAATTTTATCTCTCATATTGTCTAGTACTGATGTTTCA 2355  
DB 300 TTGCTGTTGGAATTTCTCTGCTGAATTTTATCTCTCATATTGTCTAGTACTGATGTTTCA 359  
QY 2356 GCTGAGCTCTTGAATCAGGTATAGAGCTGCTGCTCTTAACTTTGCTTTGCGAG 2415  
DB 360 GCTGAGCTCTTGAATCAGGTATAGAGCTGCTGCTCTTAACTTTGCTTTGCGAG 419  
QY 2416 TCCATTGATAATTTCCCACTCAATGTTGGCAAACTTTCCAGAGAGTACTACTGAGTTCT 2475  
DB 420 TCCATTGCAATTTCCCACTCAATGTTGGCAAACTTTCCAGAGAGTACTACTGAGTTCT 479  
QY 2476 GCAAGAAATGTTTACTACAGTACCCCACTGTTTTTAACTTTAGAAATGCTGAGTTGT 2535  
DB 480 GCCAGGATGTTGACCGCAGTCCCGCTGTTTTTCCAAAGCTGTTAACTTTGCTTAAATGCT 539  
QY 2536 TCCAGTTTCCACTCACTTCCAGAGATGCTGCGGCTTTGATGCTATTGCGAGATGAGTG 2595  
DB 540 TCTGGCTCCACCACTTCCAGAGATGCTGCGGCTTTGATGCTATTGCGGATGAGTTA 599  
QY 2596 GAAATTCGGAAGCCATCCAGTTGGCGGTAGAGACACTTTGGATGCTCAACAGGACAGC 2655  
DB 600 GAAATTCGGAAGCTCATCCAGTGGGTGGAGGACACTGTGGATGGGCTATCAGGACAG- 658  
QY 2656 TTCTTGGAGGCACTGTTTCCCACTATCTCTGGAACCACTATCTCCCTGAG 2715

Db 659 --CTTACAGCGCGTGGCCCCCACCAGCTGTCT-----AGAAAAACAGCTCCCTTGAG 707  
QY 2716 TGCACAGTCCATTTAGAGAAACTGGAAAGGATATGTGCTCAAAATTTAGTGCCAGT 2775  
Db 708 CACACAGTCCATAGAGAGAAACTGGAAAGGACTAAGTGTCTACGACGTAGTGGCCAGC 767  
QY 2776 TCAGAGAGACATTTCTGAGAGACTGGCCGAGCATTTTCAGTAGACCTTCTAGTTCAAACA 2835  
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QY 2836 ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 2895  
Db 820 -----CAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 872  
QY 2896 AGTCAGTGTGTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2955  
Db 873 AGTCAGTGTGTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 929  
QY 2956 TCAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3015  
Db 930 TCAGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 974  
QY 3016 CATAGACTTCAGGATTCATTTCCCTGCGAATACCTTTCTGATCTCTCTCTCTCTCTCT 3075  
Db 975 CACAGACCCAGGATTTGTTTCCCTGCAAAATACCTTCCGATCTCTCTCTCTCTCTCTCT 1034  
QY 3076 AAGTTCTCTACAAATCCACAGAACTGTCTCTGAAACAAAGACTCAGATAAATTTCC 3135  
Db 1035 AAGTTCTCTACAAATCCAGAGAACTGTCTCTGAAACAAAGACTCAGACCACTCTCT 1094  
QY 3136 CCAGTCTTTACTCAGTCAAGACCTTGGCCCTCCAGTAACATACACAGGCCCAAGCCATCT 3195  
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Db 1155 CGACCCGTTCCGGGAGTACAGCAAACTAGGGAGCGCCCAAAAATAGCATGACACTT 1214  
QY 3256 GATCTGAACAGTAGTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCAATAGTAGTAAT 3315  
Db 1215 GATCTGGGAGTGTCTTCAGGTGTGACGACAGCTTTGGCGGCGGCGCACAGTGGCAAC 1274  
QY 3316 GCTGTATACCCAGTGCAGACAGTGTTCACCCAGTAGAGAGAAATGACAGATTAGAT 3375  
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QY 3376 GTCATACAGAGCTCAACTCCAGTATTCAGGACCTTCTTGAAGCATCTATGSCCTTCAAGT 3435  
Db 1335 GTGAACACGAGCTCAACTCCAGCATTCAGGACCTTCTTGAAGCATCTATGSCCTTCAAGT 1394  
QY 3436 GATACAAACAGTAACCTTTTAAAGTCAGAACTTGTCTGTCTCTCTGAAAAGGCTGAAAAT 3495  
Db 1395 GACAGCAGTCACTTTTCAAGTCCGAACTGCGCGCTCTCTCTCGGAAAAGGCGGAAAAT 1454  
QY 3496 GATGATACCTCAAGATGATGTGAATCAATCAAAAGTGCAGAGAGATGGAAGCT 3555  
Db 1455 GACGACACTCAAAAGACAGCTCAATCAATCAAAAGTGCAGAGAGATGGAAGCT 1514  
QY 3556 GAAGAAGAGAGCTTTTAGCAATTCGCAATGTGAGCGTCTCAGGATGCGCCCTCCC 3615  
Db 1515 GAAGAAGAGAGCTTTTAGCGATGCGCATGCGGATGTGAGCGTCTCAGGATGCGCCCTCCC 1574  
QY 3616 ATAGTTCCTCAGCTCGAGTTGAAATGGAGAGATATCATCATTTTCAACAGATACA 3675  
Db 1575 ATCGTCCCTCAGCTCGAGTTGAAATGGAGAGATATTTATCATTTTCAACAGATACA 1634  
QY 3676 CCAGAGACTCTACAGGACATACCAAGCAAAACAACCGTATAGAGAGACACTGGAATGG 3735  
Db 1635 CCAGAGAACTCTTCCAGGACATACCAAGCAAAACAACCGTATAGAGAGACACTGGAATGG 1694  
QY 3736 CTGAAAGGTCAACAGATAGGCTTTGAGCACTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 3795  
Db 1695 CTGAAAGGTCAACAGATAGGCTTTGAGCACTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1754

QY 3796 GGAACTGGAACTTTAATGGCTTTAAACAGAGTGACTTATGTGAGAAAACACATCTTCTGAG 3855  
Db 1755 GGGACTGGGACTTTAATGGCTGTGAAAACAGAGTGACGTACGTGAGAAAACACATCTTCTGAG 1814  
QY 3856 CAAAGAGAAAGTAGTAGAGACTAAGAGAGAGATAGAAATGATGAGCCATCTGAATCAT 3915  
Db 1815 CAGGAGGAGGTGGTGAAGCGTTGAGGGAAGAGATCCGGATGATGGGTCACTCAACCAT 1874  
QY 3916 CAAAACATCATTAGGATGTTGGGAGCCAGCTGTGAGAGAGCAATTAACAATCTTCTTCAAT 3975  
Db 1875 CAAAACATCATTCGGATGCTTGGGAGCCAGCTGTGAGAGAGCAATTAACAATCTTCTTCAAT 1934  
QY 3976 GAATGATGGCAGGGGATCGGTGCTCATTTGTCTGAGTAATATGAGGCTTCAAAGAA 4035  
Db 1935 GAGTGGATGGCGGAGGATCTGTGCTCACCTCTTGTAGTAATATGAGGCTTCAAAGGAG 1994  
QY 4036 TCAGTAGTTATTAACTACACTGAAACAGTTTACTCCGTGGCTTTTCTGTCTCTCCATGAAAC 4095  
Db 1995 TCAGTCTCTATTACTACTGAGCAGTTACTGTGCTGGCTTTTCTGTCTCTCCAGGAC 2054  
QY 4096 CAAATCATTCACAGAGATGTCAAAGGTGCAATTTGTAAATTTGACAGCATGCTGTCAGAGA 4155  
Db 2055 CAGATCATTCACAGAGACGTCAAAGGTGCCAACCCTGCTCATTTGACAGCACCGGTGAGAG 2114  
QY 4156 CTAAGAAATTCAGATTTTGGAGCTGCAGCCAGGTGGCATCAAAAGGAACTGTCGAGGA 4215  
Db 2115 CTGAGAAATTCAGACTTTTGGAGCTGTGCCAGTTTGGCATCAAAAGGAACTGTCGAGGA 2174  
QY 4216 GAGTTTCAGGGAACAATTTACTGGGGAACAATTTGCAATTTATGGCACTTGAAGTACTAAGAGT 4275  
Db 2175 GAGTTTCAGGGAACAATTTACTGGGGAACAATTTGCAATTTATGGCCCTGAGGTCTTAAGAGT 2234  
QY 4276 CAAAGATTCGAAGGAGCTGTGATGTATGGAGGTGTGGCTGTCTATTATAGAAATGGCT 4335  
Db 2235 CAGCAGTATGGTAGGAGCTGTGATGTATGGAGGTGTGGCTGTCTATTATAGAAATGGCT 2294  
QY 4336 TGTGCAAAAACCACTGGAATGCAGAAAACCACTCCAATCATCTCGCTTTGATATTTAAG 4395  
Db 2295 TGTGCAAAAACCACTTGGAAATGCAGAAAACCACTCCAATCATCTCGCTTTGATATTTAAG 2354  
QY 4396 ATTGCTAGTGCAACTACTGCTCATGATCCCTTCACTTTGCTCTCTGTTTACAGAT 4455  
Db 2355 ATTGCTAGTGCAACTACTGCTCATGATCCCTTCACTTTGCTCTCTGTTTACAGAT 2414  
QY 4456 GTGGCTCTCTGTTTGTAGAACTTCAACCTCAGGACAGACCTTCCATCAAGAGAGTACTG 4515  
Db 2415 GTGGCGCTGCTGCTTAGAACTTCAAGCTCAGGACCGGCTCCCTCCAGAGAGTCTGCTG 2474  
QY 4516 AAGCATCCAGTCTTCTGTAATGATGAGTCCCAATTTAGCAGATCAACTACAGTAGAAG 4575  
Db 2475 AAACATCCGCTCTCCGTAACCGTACCGTACCGTCCCTGCTCCCGGCTTCCGCGAC 2534  
QY 4576 AGGATGCTCAACAGAGAGAAAACCTTG-----TGGGGAACCACTTGTATTTCTACTGG 4631  
Db 2535 AGGATTCGAAACCGGAGAGAGAAAGAGAACTTGTGGGCGACCATGCGCTTAAACGAG 2594  
QY 4632 CCATGATGCCATGAAACAGCTATGAACGAGGCGAGTGGGGAACCTTACCTAAGTATGTG 4691  
Db 2595 CCCTCAACGCACTGAAACAGGAGAAACGCGGCGAGCGGGAACCGTACCTAAGCATGTG 2653  
QY 4692 ATTGACAAATCATGATCTGTACTAGCTCAGTATGCA-AAAAGCCAACTAGTGCAGAA 4750  
Db 2654 ATTGACAAATCATGATCTGTACTAGCTCAGTATGCAAGCATCTACAGCTCGTGCAGGA 2713  
QY 4751 ACTGTAACCTGCTCTTCAAAGAACTGCGCTTAGGTGAACAGGAAAACAATGAAGTTTG 4810  
Db 2714 ACTGCACACCGTCTCTTCAAGGACTGCTCTGCGGAGCCAGGAAAGGCGATGGAGTTG 2773  
QY 4811 CATGACTTAATTCAGAGACATAATTTATTTTTTTTGGAGCACTTTTTCAGCAA 4864  
Db 2774 CATGACTTAAGAACAGAGCAATAATTTA-----TTTTTGGAGCACTTTTTCAGCTA 2825



Db 1575 ATCGTCCCTCAGCTGCGAGTGGAAATGGAGAGATATTATCATCTATTACAGAGACACA 1634  
Qy 3676 CCAGAGACTCTACAGGACATACCAAGCAAAACACCGTATAGAGAGACACTGAATGG 3735  
Db 1635 CCAGAAATCTCTCCAGGACATACCAAGCAAAACAGCCTTACAGAGAGACGCTGAGTGG 1694  
Qy 3736 CTGAAGGTCAACAGATAGGCTTGGAGCATTTCTTCTTGTATCAGGCTCAAGATGTG 3795  
Db 1695 CTGAAGGCCAGCAGATAGGCTCGAGCATTTCTTCTTGTATCAGGCTCAAGATGTG 1754  
Qy 3796 GGAATCTGGAATTTTAACTGCTTAAACAGAGTGACTTATGTGACAGAAACACATCTTCTGAG 3855  
Db 1755 GGGATCTGGACCTTTAACTGCTGTGAACAGGTGAGTACGTACGACAGAAACATCTCCGAG 1814  
Qy 3856 CAGAGAGATAGTATAGAGCTAAGAGAGAGATAGAGATAGAGATAGAGATAGAGATAGAGAT 3915  
Db 1815 CAGGAGAGGTGTGGAAGCGTTGAGGAGAGATCCGGATGATGGGTCACTCAACCAT 1874  
Qy 3916 CCAACATCATTTAGATGTGGAGCCACGCTGTGAGAGAGCAATTACAATCTCTTCAAT 3975  
Db 1875 CCAACATCATTTAGATGTGGAGCCACGCTGTGAGAGAGCAATTACAATCTCTTCAAT 1934  
Qy 3976 GAATCGATGGCAGGGGATCGGTGCTCATTTGTCTGAGTAATATGGAGCCTTCAAGAA 4035  
Db 1935 GAGTGGATGGCGGAGGATCTGTGGCTCACCTCTTGTGTAATATGGAGCCTTCAAGAG 1994  
Qy 4036 TCAGTATGTTATTAACATCACTGACAGTACTCTCGTGGCTTGTATCTCATGAAAC 4095  
Db 1995 TCAGTCTGCTTAACTCACTGACAGTACTCTCGTGGCTTGTATCTCATGAAAC 2054  
Qy 4096 CAAATCATTCAGAGATGTCAAGGTGCTCAATTTGTCTGAGTAATATGGAGCCTTCAAGAA 4155  
Db 2055 CAGATCATTCAGAGAGCTCAAGGTGCTCAATTTGTCTGAGTAATATGGAGCCTTCAAGAG 2114  
Qy 4156 CTAAGATTCAGATTTTGGAGCTCAGCAGGTGGATCAAAAGGAACTGGTGCAGGA 4215  
Db 2115 CTGAGATTCAGATTTTGGAGCTCAGCAGGTGGATCAAAAGGAACTGGTGCAGGA 2174  
Qy 4216 GAGTTTCAGGGAACAATTACTGGGGCAATTTGATTTATGGCACTGAGTACTAAGAGGT 4275  
Db 2175 GAGTTTCAGGGAACAATTACTGGGGCAATTTGATTTATGGCACTGAGTACTAAGAGGT 2234  
Qy 4276 CAAAGTATGGAAGAGCTGTATGTATGGAGTGTGCTGTCTATTTATAGAAATGGCT 4335  
Db 2235 CAGCAGTATGGAAGAGCTGTATGTATGGAGTGTGCTGTCTATTTATAGAAATGGCT 2294  
Qy 4336 TGTGCAAAACCACTGATGCAAGAAACCACTCCATCATCTTGTCTGATATTTAAG 4395  
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Qy 4396 ATTGCTAGTGAACCTACTGCTCCATCGATCCCTTCCATTTGTCTCTGTTTACGAGAT 4455  
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Qy 4456 GTGGCTCTCTGTTTGTAGAACTTCAACTCAGGACAGACCTTCACTCAAGAGAGCTACTG 4515  
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Qy 4516 AAGCATCCAGTCTTTCTGCTACTACATGGTAGCAATTTATGCAAGTCACTCACTAGAGAAAC 4575  
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Qy 4576 AGGATGCTCAACAGAGAAAAAACTTG- --- TGGGAAACCAATGATATTTCTACTGG 4631  
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Qy 4632 CCATGATGCCATGAAACAGCTATGAACGAGGCGAGTGGGAAACCTTACCTTAAGTATGTG 4691  
Db 2595 CCCTCAGCCATGAAACAGCTATGAACGAGGCGAGTGGGAAACCTTACCTTAAGTATGTG 2653  
Qy 4692 ATTGCAAAATCATGATCTGTACCTAAGCTCAGTATGCA- AAAGGCCAAACTAGTGCAGAA 4750  
Db 2654 ATTGCAAAATCATGATCTGTACCTAAGCTCAGTATGCA- AAAGGCCAAACTAGTGCAGAA 2713

Qy 4751 ACTGTAAACTGTGCTTTCAAGAACTGCGCCCTAGGTGAACAGGAAAAACAATCAAGTTTG 4810  
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Qy 4811 CATGACTAAATGCGAGCAAGCAATAATTTATTTTGTGGAGCACTTTTTCAGCAA 4864  
Db 2774 CATGACTAAAGAACAGAGCAATAAATTTA- -TTTTTGGAGCACTTTTTCAGCTA 2825

## RESULT 11

US-09-016-434-794  
; Sequence 794, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhammer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREMITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 794:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 226 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: HNT2NOT01  
; CLONE: 493684  
; US-09-016-434-794

Query Match 4.3%; Score 226; DB 4; Length 226;  
Best Local Similarity 100.0%; Pred. No. 2.2e-45;  
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3279 TGATGACAGCTTTGGCTGTAGCAGCAATAGTAGTAATGCTTTATACCCAGTGCAGAC 3338  
Db 1 TGATGACAGCTTTGGCTGTAGCAGCAATAGTAGTAATGCTTTATACCCAGTGCAGAC 60  
Qy 3339 AGTGTTTCAACCCAGTGCAGCAATAGTAGTAATGCTTTATACCCAGTGCAGAC 3398  
Db 61 AGTGTTTCAACCCAGTGCAGCAATAGTAGTAATGCTTTATACCCAGTGCAGAC 120  
Qy 3399 TATTGAGGACCTTTCTTGAAGCAATCTATGCTTCAAGTGTATACCAAGTAACTTTTAAGTC 3458  
Db 121 TATTGAGGACCTTTCTTGAAGCAATCTATGCTTCAAGTGTATACCAAGTAACTTTTAAGTC 180





QY 4387 ATATTAGATTGCTAGTGCACACTACTGCTCATCGATCCCTTACATTGCTCTCTGGT 4446  
Db 658 CTCCTTCCATATAGGACAAACCAATCCCATCCCATCCACAGACATCTTTCTGCTGAA 717  
QY 4447 TTACGAGATGTGGCTCTTCTGTTGTTAGAACTTCAACCTTCAGGACAGACCTCCATCAAGA 4506  
Db 718 TCAAAGGACTTCTCTATTAAATGTTTGCAGAGGAAACCGCACCTCAGGCAATCTGCACTCA 777  
QY 4507 GAGCTACTGAAGCATCCAGTCCTTT 4530  
Db 778 AATTGCTTCCAGCATCCATTTGTT 801  
RESULT 14  
US-09-371-338-20  
; Sequence 20, Application US/09371338  
; Patent No. 6613959  
; GENERAL INFORMATION:  
; APPLICANT: Sheen, Jen  
; APPLICANT: Kovtun, Yelena V.  
; APPLICANT: Chiu, Wan-Ling  
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A MAPKKK  
; TITLE OF INVENTION: PROTEIN KINASE DOMAIN  
; FILE REFERENCE: 00786/366002  
; CURRENT APPLICATION NUMBER: US/09/371,338  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 60/095,938  
; PRIOR FILING DATE: 1998-08-10  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 2527  
; TYPE: DNA  
; ORGANISM: Nicotiana tabacum  
US-09-371-338-20  
Query Match 2.3%; Score 120.4; DB 4; Length 2527;  
Best Local Similarity 50.8%; Pred. No. 3.9e-19;  
Matches 407; Conservative 0; Mismatches 376; Indels 21; Gaps 4;  
QY 3733 TGGCTGAAAGGTCAACAGATAGGCGCTTGGAGCATTTTCTTCTTGTATCAGGCTCAAGAT 3792  
Db 290 TGGAGAAAGGTGAATGATGCTGTGCTTTTGGTAGGTTTATATGGGATGAAT 349  
QY 3793 GTGGGAACCTGAATCTTAACTGCTTTAAACAGGTGACTTATGTCAAGAACACATCTTCT 3852  
Db 350 GTTGAATCTGGAGAGTTACTCGCTATAAAGGAGGTTTCGATTCCGATGAATCGTCTCG 409  
QY 3853 GAGCAAGAAGAGTAGTAGA-----AGCACTAAGAGAAGAGATAAGATGATGAGCCAT 3906  
Db 410 AGAGAGCGAGCAACAGCTCATGTTAGAGAGCTTGGAGAGAGTGAATCTATTGAAGAT 469  
QY 3907 CTGAATCATCCAAACATCATAGATGTTGGAGAGCCAGGTGTGAGAGAGCAATTAACAT 3966  
Db 470 CTCTCCCATCCCAACATGATGAGATATTGGGAACCTGCAAGAGAGCGAGATCATTAAT 529  
QY 3967 CTCTTCATTAAGTGGAGGAGGAGTGGTGGCTCATTTGCTGAGTAAATATGAGGC 4026  
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QY 4027 TTCAAAGAATCAGTAGTATTATACTACATCAAGAGTTACTCGTGGCCCTTTCGATATTC 4086  
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Db 650 CATAGAATGGGATTATGACAGAGATATTAGGAGAGCAACATCTTGTTCATATAA 709  
QY 4147 GGTCAAGACTAAGAATTCAGATTTTGGAGCTGCAGCCAGGTGGCATCAAAAGGAAT 4206  
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QY 4207 GGTGCAGAGAGTTTACGGACAAATTTACTGGGACAAATTCATTTTATGGCACCTGAGTA 4266

Db 767 ATGACTGTGCCAAGTC-----AATGAAGGTACTCCATCTACTGATGGCTCCGAGTC 820  
QY 4267 CTAAGAGGTCAACAGATGGAAGAGCTGTGATGTATGGAGTGTGTGGCTGTGCTATTATA 4326  
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QY 4327 GAAATGCTTGTCCAAAACCCACCATGGAATGCAGAAAAACACCTCCATCATCTTCTTTG 4386  
Db 881 GAAATGGCTACAGAAAAACCTCTTGA-----GCCAGCATATCAGGAGTTGCTGCT 934  
QY 4387 ATATTTAAGATTTGCTAGTGCACACTACTGCTCCATCGATCCCTTTCACATTTGTCTCTGGT 4446  
Db 935 CTCTTCCATATAGGCAACAAATCCATCCCATCCAGAGCATCTTTCTGCTGAA 994  
QY 4447 TTACGAGATGTGGCTCTTCTGTTGTTAGAACTTCAACCTTCAGGACAGACCTCCATCAAGA 4506  
Db 995 TCAAAGGACTTCTCTATTAAATGTTTGCAGAGAAACCGCACCTCAGGCAATCTGCACTCA 1054  
QY 4507 GAGCTACTGAAGCATCCAGTCCTTT 4530  
Db 1055 AATTGCTTCCAGCATCCATTTGTT 1078  
RESULT 15  
US-09-371-338-14  
; Sequence 14, Application US/09371338  
; Patent No. 6613959  
; GENERAL INFORMATION:  
; APPLICANT: Sheen, Jen  
; APPLICANT: Kovtun, Yelena V.  
; APPLICANT: Chiu, Wan-Ling  
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A MAPKKK  
; TITLE OF INVENTION: PROTEIN KINASE DOMAIN  
; FILE REFERENCE: 00786/366002  
; CURRENT APPLICATION NUMBER: US/09/371,338  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 60/095,938  
; PRIOR FILING DATE: 1998-08-10  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 804  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-371-338-14  
Query Match 2.2%; Score 117.2; DB 4; Length 804;  
Best Local Similarity 50.4%; Pred. No. 1.2e-18;  
Matches 405; Conservative 0; Mismatches 378; Indels 21; Gaps 4;  
QY 3733 TGGCTGAAAGGTCAACAGATAGGCGCTTGGAGCATTTTCTTCTTGTATCAGGCTCAAGAT 3792  
Db 13 TGGCGGAAAGGTCAAGTAAATTTGGCGCTTGGTACTGTGTAATATGGGTATGAAT 72  
QY 3793 GTGGGAACTGGAACCTTTAATGGCTGTAAACAGGTGACTTATGTCAAGAAACACATCTTCT 3852  
Db 73 CTCGATTCGGGTGAGCTTCTCGCGTTAAACAGGCTCTGATTACATCTAATTGTGCATCC 132  
QY 3853 GAGCAAGAGAGTAG-----TAGAAGCACTAAGAGAGAGATAAGAAATGATGAGCCAT 3906  
Db 133 AAGGAAAAAATCTCAGGCTCATATTTCAGAGCTTGAAGAGGAGTGAAGTACTACTCAAGAT 192  
QY 3907 CTGAATCATCCAAACATCATTAGGATGTTGGAGCCACAGTGTGAGAGAGCAATTAACAT 3966  
Db 193 CTCCTCATCCAAATATAGTTAGATATTGGGTACGTTGAGGAGAGATGAACTTTGAAT 252  
QY 3967 CTCCTCATTAATGATGAGGAGGAGTGGTGGCTCATTTGCTGAGTAATATGGAGCC 4026  
Db 253 ATCTTGTGTAATTTGTTCTCTGGTGGATCTATATCTTCACTCTTTGGGAAATTTGGAGCC 312  
QY 4027 TTCAAAGAATCAGTAGTATTATACTACATCAAGAGTTACTCCGTCGCTTTCGATCTC 4086

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Db 313 TTTCCTGAATCTGTTGTTGGGACATACACGACCAACTGCTTTTGGGATTGGAGTACCTT 372
QY 4087 CATGAAACCAAAATCATTCACAGAGATGTCAAAAGTGCCTTAATTTGCTTAATTCAGACACT 4146
Db 373 CATAATCATGCGCAATATGACCGTGACATTAAGGGTGTCTAATATCCCTTGTGGATAATCAA 432
QY 4147 GGTACAGAGACTAAGAAATTCAGATTTTGGAGCTGCAGCCAGGTTGGCATCAAAAAGGAACT 4206
Db 433 GG--ATGCATTAAACTTTGCTGATTTTGGTGGCTCCAAACAGGTAGCGGAGTTGGCTACT 489
QY 4207 GGTGAGGAGAGTTTCAGGGACAATTAATCTGGGACAATTCATTTATGGCACCTTGAGGTA 4266
Db 490 ATTCGGGTGCCAAATCTATGAAA-----GGAACTCCCTATTGGATGGCTCCAGAAAGTT 543
QY 4267 CTAAGAGGTCAACAGTATGGAAGGAGCTGTGATGTATGGAGTGTGGCTGTGCTATTATA 4326
Db 544 ATCTTCAAAACCGGGCATAGCTTTTCTGCTGATATTTGGAGTGTAGGATGCACAGTGATT 603
QY 4327 GAAATGGCTTTGCAAAACCAACCATGGAAATGCAGAAAAACACTCCAATCATCTTCTCTTG 4386
Db 604 GAAATGGTGAATGGAAGCTCCTTGA-----GCCAGCAATATAAAGAGATTGCTGCT 657
QY 4387 ATATTAGATTGCTAGTCAACTACTGCTCCATCGATCCCTTCACATTTTGTCTCTGCT 4446
Db 658 ATTTTCCCATTTGGAAACGACGAATGCGATCTCCAAATCCCTGACAATATCTCCTCTGAC 717
QY 4447 TTACGAGATGTGGCTCTTCTGTTGTTTGTAGAACTTCAACCTCAGGACAGACCTCCATCAA 4506
Db 718 GCAATATGATTTTGTCTCAAGTGTCTGACAGAGAACCAAAATCTCGGCGCAACCGCTTCT 777
QY 4507 GAGCTACTGAAGCATCCAGTCTTT 4530
Db 778 GAGCTGCTAAAGCATCCATTGTT 801
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Search completed: May 15, 2004, 04:19:45  
Job time : 336 secs



PI Yue H, Ding L, Lal PG, Griffin JA, Gururajan R, Baughin MR;  
PI Ison CH, Ramkumar J, Tribouley CM, Swannakar A, Burford N;  
PI Bandman O, Thornton M, Khan FA, Walla NK, Nguyen DB, Elliott VS;  
XX Xu Y, Lu Y, Hafalia AJA, Yao MG, Gandhi AR, Arvizu C, Forsythe I;  
DR WPI; 2002-519665/55.  
DR P-PSDB; RAE25086.  
XX  
XX Novel human kinase and phosphatase polypeptide, useful in diagnosis,  
PT prevention or treatment of cardiovascular, immune system, neurological,  
PT growth, developmental, lipid and cell proliferative disorders.  
XX  
XX Claim 81; Page 202-203; 219pp; English.  
XX  
XX The present invention relates to novel human kinase and phosphatase (KAP)  
CC proteins and polynucleotides encoding such proteins. Sequences of the  
CC invention are useful for treating or preventing disorders associated with  
CC aberrant expression of KAP where the disorders include cardiovascular  
CC disorders (e.g., atherosclerosis, hypertension, vasculitis), immune  
CC system disorders (e.g., acquired immunodeficiency syndrome (AIDS), gout,  
CC anaemia, asthma, diabetes mellitus, multiple sclerosis), neurological  
CC disorders (e.g., epilepsy, stroke, Alzheimer's disease, Huntington's  
CC disease, Parkinson's disease), growth and developmental disorders (e.g.,  
CC cirrhosis, hepatitis, prolatias), lipid disorders (e.g., fatty liver,  
CC Gaucher's disease, obesity) and cell proliferative disorders (e.g.,  
CC arteriosclerosis, myelofibrosis and cancer). They are useful for drug  
CC screening techniques and to analyse the proteome of a tissue or cell  
CC type. KAP sequences are useful for creating knock-in humanised animals or  
CC transgenic animals to model human diseases, in somatic or germline gene  
CC therapy, to generate a transcript image of a tissue or cell type, for  
CC detecting differences in the chromosomal location due to inversion, or  
CC translocation among normal, carrier or affected individuals and as  
CC hybridisation probes for mapping naturally occurring genomic sequences.  
XX The present sequence is human KAP-6 cDNA

SQ Sequence 4858 BP; 1374 A; 1140 C; 1192 G; 1152 T; 0 U; 0 Other;

Query Match 90.5%; Score 4744.8; DB 6; Length 4858;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 4793; Conservative 0; Mismatches 22; Indels 5; Gaps 3;

QY 7 ATGGCGCGCGCGCGGGAATCGCGCTCGTCTCGTGGGATTCGCCGGGCCAGCGGCTACG 66  
DB 1 ATGGCGCGCGCGCGGGAATCGCGCTCGTCTCGTGGGATTCGCCGGGCCAGCGGCTACG 60  
QY 67 AGCCCTGAGCAGCGCGCGCGGAGAGCCCTCAAGGCGAGCAGCGCGCGCGCTGCC 126  
DB 61 AGCCCTGAGCAGCGCGCGCGGAGAGCCCTCAAGGCGAGCAGCGCGCGCGCTGCC 120  
QY 127 GCGGGAAGTGTGCGGAGCGCGGCGAGCGGCGCGGCGGCGGCGGCGGCGGCGG 186  
DB 121 GCGGGAAGTGTGCGGAGCGCGGCGAGCGGCGCGGCGGCGGCGGCGGCGGCGG 180  
QY 187 CAGCTCGGCAAGTGTGCGGAGTGTGAGCTGGAACAGCTGCTGAGCAGCGCTCTTCCTT 246  
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QY 247 GCGGCTCACCGCGCGCTCTTCGACTTCCCGCTGCGCGGAGCGCGGCGGCGGCGGCGG 306  
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QY 307 AGTGGAGACGGCTTTCAGCCTGTGCGGCTGTGCGCGCGCGCGCGCGCGCGCGCGCG 366  
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QY 367 GCGGCGCGCGCTTACCGAGTGTGCGGCGCGCGGAGCGCGGCGCGCTTCGAGTCCCGCAGCG 426  
DB 361 GCGGCGCGCGCTTACCGAGTGTGCGGCGCGCGGAGCGCGGCGCGCTTCGAGTCCCGCAGCG 420  
QY 427 GCGGAGCGCGGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 486  
DB 421 GCGGAGCGCGGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480

QY 487 GGTCTGTGAGTGGAGCAATAAAGAACTCTCAAAGGTTGCAACAAGATGATGATCGTCCA 546  
DB 481 GGTCTGTGAGTGGAGCAATAAAGAACTCTCAAAGGTTGCAACAAGATGATGATCGTCCA 540  
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DB 541 GAGGAACGAATGATCAGGAGAACTGAAGCAACCTGTATGCCAGCTGGAACGAGAA 600  
QY 607 TGGTTGGAAGGAGAAATAGCGAGGCGCTGTGGTGTAAACCAATCCCAAGTTAAAGGA 666  
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DB 661 GATGATCTGAAATCAATCTTAGCAGCTGAGTCTCCAGAGAGCTCCAGGCAAGTGG 720  
QY 727 GCTTACCAAGCTTCAAAGGCGCGAGTCTCTCTCTGCGCAATCCCAATCAGGTGCG 786  
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QY 847 AGTGGCAGAAATCACACCCCGAAGAGCCCTTCCAGAGTGGCTTCTCACCATATAGC 906  
DB 841 AGTGGCAGAAATCACACCCCGAAGAGCCCTTCCAGAGTGGCTTCTCACCATATAGC 900  
QY 907 CCGTGAAGAAACAAACCGCGGTGTTTAAAGTGTGCGGCGGCGAGTCTTACTTCTGCGAG 966  
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DB 1141 AAGAAATTTTGTGAGTTGAGAGTTTGTTCAGAAATATCAAGTAGGCGTGTCTCAAGATC 1200  
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DB 1201 AAGCTCCATCTCGTAACACCATCCAGAGTTTGTTCAGCATGTCAAATTTCTCATACA 1260  
QY 1267 TTGTTCATCTAGTACTTCTACGTCTGTAGTTCAAGAAACAGCATATAAGGATGAAGAGAA 1326  
DB 1261 TTGTTCATCTAGTACTTCTACGTCTGTAGTTCAAGAAACAGCATATAAGGATGAAGAGAA 1320  
QY 1327 CAGATGCTCTATTTGCTTTGGGCGATGTTGAGTGAAGAGAGTCTTACAGTGTGTGAA 1386  
DB 1321 CAGATGCTCTATTTGCTTTGGGCGATGTTGAGTGAAGAGAGTCTTACAGTGTGTGAA 1380  
QY 1387 GACGGCTGCGAGGAACAAGCTGCGACCACTCGCATGTCAAATTTGGGCGAAGAGTGTAGA 1446  
DB 1381 GACGGCTGCGAGGAACAAGCTGCGACCACTCGCATGTCAAATTTGGGCGAAGAGTGTAGA 1440  
QY 1447 AGAAATAGAGAACCTTTAATATGTCCCTTTGTAGATCTAAGTGGAGATCTCATGATTTTC 1506  
DB 1441 AGAAATAGAGAACCTTTAATATGTCCCTTTGTAGATCTAAGTGGAGATCTCATGATTTTC 1500  
QY 1507 TACAGCCACAGATGTCAAGTCTCTGTGGATTCCCTTTCTTCCCTCAGAGTGCACAGCAG 1566  
DB 1501 TACAGCCACAGATGTCAAGTCTCTGTGGATTCCCTTTCTTCCCTCAGAGTGCACAGCAG 1560  
QY 1567 CAACACCGTACAGCAGCAGCTTTGGCTGGATCAGAAAGAAATCAAGAGAGCAATTTTAAAC 1626

1561 CAAACCGTACAGCAGCAGCCTTTGGCTGGATCAGGAAGAAATCAAGAGAGCAATTTTAAAC 1620  
1627 CTTACTCATTTATGGAAGTCAAGCAATCCCTCCTGCTTTACAAAGATTTAGCTGAGCCATGG 1686  
1621 CTTACTCATTTATGGAATCTAGCAAAATCCCTCCTGCTTTACAAAGATTTAGCTGAGCCATGG 1680  
1687 ATTCAAGTGTGTTGGAATGGAACCTGTTGGCTGCTTTATTTCTAGAAAACCTGGAATGTGAGA 1746  
1681 ATTCAAGTGTGTTGGAATGGAACCTGTTGGCTGCTTTATTTCTAGAAAACCTGGAATGTGAGA 1740  
1747 GAGATGCCCTCAGGCGCTCTTTCCCATGATGTAGTGGGGCCCTGCTGTTGGCAAAATGGG 1806  
1741 GAGATGCCCTCAGGCGCTCTTTCCCATGATGTAGTGGGGCCCTGCTGTTGGCAAAATGGG 1800  
1807 GAGAGCACTGGAATTTCTGGGGGAGCAGAGTGGAGAGCCCGAGTGGGGAGCCACCAAGT 1866  
1801 GAGAGCACTGGAATTTCTGGGGGAGCAGAGTGGAGAGCCCGAGTGGGGAGCCACCAAGT 1860  
1867 GGGTCTTCCAGACAGCATGATCTCAGGAGATGTGGTGAGGCATGCTGCAGCGTTCTGTCA 1926  
1861 GGGTCTTCCAGACAGCATGATCTCAGGAGATGTGGTGAGGCATGCTGCAGCGTTCTGTCA 1920  
1927 ATGCTGTGCTGACCCCTGCTCAAAAGTGTACGTTGCTGCTTTAAAAACATTTGAGAGCC 1986  
1921 ATGCTGTGCTGACCCCTGCTCAAAAGTGTACGTTGCTGCTTTAAAAACATTTGAGAGCC 1980  
1987 ATGCTGTGATATACCTCTGTCACAGTTTACGGAAGAAAGATCAAACTTCAGAGACTTCTC 2046  
1981 ATGCTGTGATATACCTCTGTCACAGTTTACGGAAGAAAGATCAAACTTCAGAGACTTCTC 2040  
2047 CAGCCAGTGTGAGACACATCCTAGTCAATGTGCAGATGCCAATGCCCAACAAGTCAG 2106  
2041 CAGCCAGTGTGAGACACATCCTAGTCAATGTGCAGATGCCAATGCCCAACAAGTCAG 2100  
2107 CTGTCCATATCAACACTGTTGGAATCTGTGCAAAAGGCCAAGCAGAGAGTTGGCAGTTGGC 2166  
2101 CTGTCCATATCAACACTGTTGGAATCTGTGCAAAAGGCCAAGCAGAGAGTTGGCAGTTGGC 2160  
2167 AGAGAAATCTAAAGCTGGATCATTTGGTATTTGGTGTGATGATGCTTTAAATTTGT 2226  
2161 AGAGAAATCTAAAGCTGGATCATTTGGTATTTGGTGTGATGATGCTTTAAATTTGT 2220  
2227 ATCTCTGGAACCCAACTGAAATCAAACTGGAAGAACTTCTTGCCGCCCTTTGTCCT 2286  
2221 ATCTCTGGAACCCAACTGAAATCAAACTGGAAGAACTTCTTGCCGCCCTTTGTCCT 2280  
2287 ATAGATAGACTGTTGTTGGAATTTCTGCTGAAATTTTATCCTCATATGTGCTACTGAT 2346  
2281 ATAGATAGACTGTTGTTGGAATTTCTGCTGAAATTTTATCCTCATATGTGCTACTGAT 2340  
2347 GTTTCACAGCTGAGCCCTGTTGAAATCAGGATTAAGAGCTGCTGTGCTCCTTTAACTTTT 2406  
2341 GTTTCACAGCTGAGCCCTGTTGAAATCAGGATTAAGAGCTGCTGTGCTCCTTTAACTTTT 2400  
2407 GCTTTGCAAGTCAATGATTAATCCCACTCAATGTTGGCAAACTTTCGAGAGATCTAC 2466  
2401 GCTTTGCAAGTCAATGATTAATTTCCCACTCAATGTTGGCAAACTTTCGAGAGATCTAC 2460  
2467 TTGAGTCTCGAAGAAATGTTTACTACAGTACCCCATGTTTTCAAAACCTGTTAGAAATG 2526  
2461 TTGAGTCTCGAAGAAATGTTTACTACAGTACCCCATGTTTTCAAAACCTGTTAGAAATG 2520  
2527 CTGAGTGTGTTCAAGTTCACATCACTTCCAGGATGCGTGCCTGTTGATGGCTATTGCA 2586  
2521 CTGAGTGTGTTCAAGTTCACATCACTTCCAGGATGCGTGCCTGTTGATGGCTATTGCA 2580  
2587 GATGAGTGGAAATTTGCCGAAGCCATCCAGTTGGCGGTAGAGACACTTTTGGATGGTCAA 2646  
2581 GATGAGTGGAAATTTGCCGAAGCCATCCAGTTGGCGGTAGAGACACTTTTGGATGGTCAA 2640  
2647 CAGGACAGCTTCTTCAGGCACTCTGTTCCCAACCACTATCTGGAACCCACAGAGACAGT 2706

2641 CAGGACAGCTTCTTCAGGCACTCTGTTCCCAACAACATATCTGGAACCCACAGAGACAGT 2700  
2707 TCCCTGAGTGCACAGTCCATTTAGAGAAAACCTGGAAGAGGATATGCTGTACAAAATTG 2766  
2701 TCCCTGAGTGCACATTCATTTAGAGAAAACCTGGAAGAGGATATGCTGTACAAAATTG 2760  
2767 AGTGCCAGTTCAGAGGACATTTCTTGAGAGACTGGCCGACATTTGAGTAGGACCTTCTAGT 2826  
2761 AGTGCCAGTTCAGAGGACATTTCTTGAGAGACTGGCCGACATTTGAGTAGGACCTTCTAGT 2820  
2827 TCAACAAACAAACAAACAAACAAACAGAGCAACCAAGCCCAATGGTTCAAAACAAAGGC 2886  
2821 T----CAACAAACAAACAAACAAACAGAGCAACCAAGCCCAATGGTTCAAAACAAAGGC 2877  
2887 AGACCCCAAGTGTGTTGAACTCTCTCTCTTTATCTCATCATTTCCCAATTTAATGTTT 2946  
2878 AGACCCCAAGTGTGTTGAACTCTCTCTCTTTATCTCATCATTTCCCAATTTAATGTTT 2937  
2947 CCAGCCCTGTCAACCCCTTCTTCTTACCCCATCTGTACCAGCTGGGACCTGCAACAGAT 3006  
2938 CCAGCCCTGTCAACCCCTTCTTCTTACCCCATCTGTACCAGCTGGGACCTGCAACAGAT 2997  
3007 GTCTCTAAGCATAGACTTTCAGGGAATTCATTCCTGCAAGATPACCTTTGTGCATCTCCTCAA 3066  
2998 GTCTCTAAGCATAGACTTTCAGGGAATTCATTCCTGCAAGATPACCTTTGTGCATCTCCTCAA 3057  
3067 ACACAGCCGAGTGTCTCTACAAATCCACAGAACTGCTCCTGAAAACAAAGACTTCAGAT 3126  
3058 ACACAGCCGAGTGTCTCTACAAATCCACAGAACTGCTCCTGAAAACAAAGACTTCAGAT 3117  
3127 AAACTTTCCCAAGTCTTTACTCAGTCAAGACCCTTTGCCCTCCAGTAAACATACACAGGCCA 3186  
3118 AAACTTTCCCAAGTCTTTACTCAGTCAAGACCCTTTGCCCTCCAGTAAACATACACAGGCCA 3177  
3187 AAGCCATCTAGACTTACCCGAGTAATACAGTAACAGGGAGATCCCTCCTCAAAAATAGC 3246  
3178 AAGCCATCTGAGACTTACCCGAGTAATACAGTAACAGGGAGATCCCTCCTCAAAAATAGC 3237  
3247 ATGACACTTGAATCTCAACAGTAGTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCAAT 3306  
3238 ATGACACTTGAATCTCAACAGTAGTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCAAT 3297  
3307 AGTAGTAATGCTGTTATATCCCGAGTGCACAGACAGTGTTCACCCAGTGTAGAGGAAATGC 3366  
3298 AGTAGTAATGCTGTTATATCCCGAGTGCACAGACAGTGTTCACCCAGTGTAGAGGAAATGC 3357  
3367 AGATTAGATGTCAATACAGAGCTCAACTCCAGTATTTAGGACCTTCTTTGAAGCATCTATG 3426  
3358 AGATTAGATGTCAATACAGAGCTCAACTCCAGTATTTAGGACCTTCTTTGAAGCATCTATG 3417  
3427 CTTTCAAGTGATACAAAGTAACTTTTAAAGTCAGAAAGTGTGCTGCTGCTCCTGAAAAG 3486  
3418 CTTTCAAGTGATACAAAGTAACTTTTAAAGTCAGAAAGTGTGCTGCTGCTCCTGAAAAG 3477  
3487 GCTGAAAATGATGATACCTTACAAAGATGATGTAATCAATCAAAAAGTCAAGAGAGAG 3546  
3478 GCTGAAAATGATGATACCTTACAAAGATGATGTAATCAATCAAAAAGTCAAGAGAGAG 3537  
3547 ATGGAAGCTGAAGAGAGAGCTTTAGCAATTTGCAATGCGCAATGTACGCGTCTCAGGAT 3606  
3538 ATGGAAGCTGAAGAGAGAGCTTTAGCAATTTGCAATGCGCAATGTACGCGTCTCAGGAT 3597  
3607 GCGCTCCCATAGTCTCAGCTGAGGTTGAAAATGGAGAGATATCATCATTTATCAA 3666  
3598 GCGCTCCCATAGTCTCAGCTGAGGTTGAAAATGGAGAGATATCATCATTTATCAA 3657  
3667 CAGGATACACAGAGACTCTACAGGACATACCAAGCAAAAACACCGTATAGAGAGAC 3726  
3658 CAGGATACACAGAGACTCTACAGGACATACCAAGCAAAAACACCGTATAGAGAGAC 3717  
3727 ACTGAATGCTGAAGGTCAAAGATAGGCTTGGAGCAATTTCTTCTGTTATCAGGCT 3786  
3718 ACTGAATGCTGAAGGTCAAAGATAGGCTTGGAGCAATTTCTTCTTCTTATCAGGCT 3777





of the invention has cardiant, antiarteriosclerotic, hypotensive, immunosuppressive, dermatological, anorectic, cytotatic, antidiabetic, haemostatic, anti-HIV, antischismatic, antibacterial, virucide, neuroprotective, nootropic, antiparkinsonian, and antilipidemic activity. A polynucleotide encoding a polypeptide of the invention may have a use in gene therapy, and as a vaccine. A polypeptide of the invention is useful in the manufacture of a medicament for treating a syndrome associated with a human disease, the disease selected from a pathology associated with the polypeptide. These may also be used in diagnosing, treating or preventing NOVX-associated disorders such as cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes, haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease, multiple sclerosis, infections, anorexia, cancer-associated cachexia, neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's disease), haematopoietic disorders, dyslipidaemias and other wasting disorders associated with chronic diseases. The nucleic acids are also used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. The present sequence encodes a NOVX polypeptide of the invention.

SQ Sequence 4840 BP; 1357 A; 1154 C; 1196 G; 1133 T; 0 U; 0 Other;

Query Match 90.3%; Score 4737.8; DB 9; Length 4840;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 4771; Conservative 0; Mismatches 12; Indels 6; Gaps 2;

|    |     |                                                             |     |
|----|-----|-------------------------------------------------------------|-----|
| QY | 1   | GAGAAATGGCGCGCGCGCGGGAATCGCGCTCGTCTGGGATTCGCGGCGCCAGG       | 60  |
| DB | 55  | GAGAAATGGCGCGCGCGGGAATCGCGCTCGTCTGGGATTCGCGGCGCCAGG         | 114 |
| QY | 61  | GCTACGAGCCCTGAGCGAGCGCGCGGAGAGCCCTCAAGCGGAGCAGCGCGCGCG      | 120 |
| DB | 115 | GCTACGAGCCCTGAG---CAGCGCGCGGAGAGGCGCCCTCAAGCGGAGCAGCGCGCGCG | 171 |
| QY | 121 | GCTGCGCGCGGACTGCTCGGAGCGCGCGGAGCGCGGCTCGCGAGCGCGGACTGG      | 177 |
| DB | 172 | GCTGCGCGCGGACTGCTCGGAGCGCGCGGAGCGCGGCTCGCGAGCGCGGACTGG      | 231 |
| QY | 178 | CGGCGCGCGAGCTGCGGAAAGTGGGAGTGGAGCTGGACAGCTGCTGAGCAGCG       | 237 |
| DB | 232 | CGGCGCGCGAGCTGCGGAAAGTGGGAGTGGAGCTGGACAGCTGCTGAGCAGCG       | 291 |
| QY | 238 | CTCTTCTTGGCGCTCACCGCGGCTCTCGACTTCCCGTCCCGGAGCGCGCGGAC       | 297 |
| DB | 292 | CTCTTCTTGGCGCTCACCGCGGCTCTCGACTTCCCGTCCCGGAGCGCGCGGAC       | 351 |
| QY | 298 | GCAGCGGAGTGGGACCGGCTTCCAGCTGTGGCGGTGCGCGCGCGCGCGCGCG        | 357 |
| DB | 352 | GCAGCGGAGTGGGACCGGCTTCCAGCTGTGGCGGTGCGCGCGCGCGCGCGCG        | 411 |
| QY | 358 | AGCGCGCGCGCGCGCGCTTACCGAGTGGGCGCGCGCGCGCGCGCGCGCGCG         | 417 |
| DB | 412 | AGCGCGCGCGCGCGCGCTTACCGAGTGGGCGCGCGCGCGCGCGCGCGCGCG         | 471 |
| QY | 418 | CCGCGAGCGCGCGCGCGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG         | 477 |
| DB | 472 | CCGCGAGCGCGCGCGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG         | 531 |
| QY | 478 | GCCTCCCGCGCTGAGTGGAGTAAAGAACTCTCAAGGGTTCACAGATGGAT          | 537 |
| DB | 532 | GCCTCCCGCGCTGAGTGGAGTAAAGAACTCTCAAGGGTTCACAGATGGAT          | 591 |
| QY | 538 | GATCGTCCAGGAGAGTATGATGAGGAGAGAACTGAAGGCAACCTGTATGCCACCTGG   | 597 |
| DB | 592 | GATCGTCCAGGAGAGTATGATGAGGAGAGAACTGAAGGCAACCTGTATGCCACCTGG   | 651 |
| QY | 598 | AAGCAGCAATGGTGGAAAGAGAAATAGCGAGCGCGCTGTGTGTTAAACCAATCCCA    | 657 |
| DB | 652 | AAGCAGCAATGGTGGAAAGAGAAATAGCGAGCGCGCTGTGTGTTAAACCAATCCCA    | 711 |
| QY | 658 | GTTTAAAGGAGATGGAATCAATCACTTAGCAGCTGAGCTCTCAAGGAGAGCTCCAG    | 717 |

|    |      |                                                             |      |
|----|------|-------------------------------------------------------------|------|
| DB | 712  | GTTTAAAGGAGATGGAATCAATCACTTAGCAGCTGAGCTCTCCAGGAGAGGTCCAG    | 771  |
| QY | 718  | GCAAGTGGCGCTTCCAGGCTTCCAAAGCGGAGCGCTCTCTCTCTGGGCACTCCCA     | 777  |
| DB | 772  | GCAAGTGGCGCTTCCAGGCTTCCAAAGCGGAGCGCTCTCTCTCTGGGCACTCCCA     | 831  |
| QY | 778  | TCAGGTTCGACAGTGAATTCAGAAATCTCCAGGAGTAAAGGAGGAGGTTTCCCAAGT   | 837  |
| DB | 832  | TCAGGTTCGACAGTGAATTCAGAAATCTCCAGGAGTAAAGGAGGAGGTTTCCCAAGT   | 891  |
| QY | 838  | CTTTTTCAGAGTGGCGAGATCACACCCCGGAGGCGCTTCCAGGAGGCTTCTCA       | 897  |
| DB | 892  | CTTTTTCAGAGTGGCGAGATCACACCCCGGAGGCGCTTCCAGGAGGCTTCTCA       | 951  |
| QY | 898  | CCATATAGCCCTGAGGAAACAAACCGCGCTGTAAACAAAGTATCGGCGCAGCTGAT    | 957  |
| DB | 952  | CCATATAGCCCTGAGGAAACAAACCGCGCTGTAAACAAAGTATCGGCGCAGCTGAT    | 1011 |
| QY | 958  | TTACTCAGAGATAGGCGCTAACTCTTCTCTGATGAGGAGAGCAGCGGAGCAATAA     | 1017 |
| DB | 1012 | TTACTCAGAGATAGGCGCTAACTCTTCTCTGATGAGGAGAGCAGCGGAGCAATAA     | 1071 |
| QY | 1018 | TACCGGCTGTTTATTTGGGCTCAGAACTGCACTGCACTGCACTGCACTTCTGTATTCAT | 1077 |
| DB | 1072 | TACCGGCTGTTTATTTGGGCTCAGAACTGCACTGCACTGCACTTCTGTATTCAT      | 1131 |
| QY | 1078 | CTCTATTTGTGATGCTCCGGTGTTCAACTAGAACCTTCAGACCCATGTTATGAGA     | 1137 |
| DB | 1132 | CTCTATTTGTGATGCTCCGGTGTTCAACTAGAACCTTCAGACCCATGTTATGAGA     | 1191 |
| QY | 1138 | AAACCTTTAAAGAAATTTGAGGTTGAGAGTTTGTCCAGAAATATCACTAGTAGCGTAGC | 1197 |
| DB | 1192 | AAACCTTTAAAGAAATTTGAGGTTGAGAGTTTGTCCAGAAATATCACTAGTAGCGTAGC | 1251 |
| QY | 1198 | TCAGGATCAAGCTCCATCTCGTAAACACATCCAGAGTTTGTTCAGCGATGTCAAT     | 1257 |
| DB | 1252 | TCAGGATCAAGCTCCATCTCGTAAACACATCCAGAGTTTGTTCAGCGATGTCAAT     | 1311 |
| QY | 1258 | TCTCATACATGTCATCTAGTCTCTAGCTAGTTTCAGAAACAGCAATAAAGGAT       | 1317 |
| DB | 1312 | TCTCATACATGTCATCTAGTCTCTAGCTAGTTTCAGAAACAGCAATAAAGGAT       | 1371 |
| QY | 1318 | GAAGAGAACAGATGTCTATTTGCTTTGGGCGATGCTTGATGAAGAAAGTCTTACA     | 1377 |
| DB | 1372 | GAAGAGAACAGATGTCTATTTGCTTTGGGCGATGCTTGATGAAGAAAGTCTTACA     | 1431 |
| QY | 1378 | GTGTGTGAACCGCTCGCAGGACAGCTGCACCACTGCATGTCATTTGGGCGAGAA      | 1437 |
| DB | 1432 | GTGTGTGAACCGCTCGCAGGACAGCTGCACCACTGCATGTCATTTGGGCGAGAA      | 1491 |
| QY | 1438 | GAGTGTAGAAAGAAATAGAGAACCTTTAATATGTCCCTTTGTAGATCTAAGTGAGATCT | 1497 |
| DB | 1492 | GAGTGTAGAAAGAAATAGAGAACCTTTAATATGTCCCTTTGTAGATCTAAGTGAGATCT | 1551 |
| QY | 1498 | CATGATTTTCAGCGCACGATGTCAGTCTGTGTGATTTCCCTTCTTCCCTCAGAGCT    | 1557 |
| DB | 1552 | CATGATTTTCAGCGCACGATGTCAGTCTGTGTGATTTCCCTTCTTCCCTCAGAGCT    | 1611 |
| QY | 1558 | GCACAGCAGCAACCGCTACAGCAGCAGCTTTGGCTGGATCAGCAAGGAATCAAGAGAGC | 1617 |
| DB | 1612 | GCACAGCAGCAACCGCTACAGCAGCAGCTTTGGCTGGATCAGCAAGGAATCAAGAGAGC | 1671 |
| QY | 1618 | AATTTTAACTTACTCATTTATGGAATCTCAGAAATCCCTCTCTTCTTCAAGATTTAGCT | 1677 |
| DB | 1672 | AATTTTAACTTACTCATTTATGGAATCTCAGAAATCCCTCTCTTCTTCAAGATTTAGCT | 1731 |
| QY | 1678 | GAGCATGGAATTCAGGTTTGTGAATCGTGTGGCTGCTTATTTTCTAGAAACTGG      | 1737 |
| DB | 1732 | GAGCATGGAATTCAGGTTTGTGAATCGTGTGGCTGCTTATTTTCTAGAAACTGG      | 1791 |
| QY | 1738 | AATGTGAGAGATGCGGCTCAGCGCTTTTCCCATGATGTCAAGGCGGCTGCTGTTG     | 1797 |
| DB | 1792 | AATGTGAGAGATGCGGCTCAGCGCTTTTCCCATGATGTCAAGGCGGCTGCTGTTG     | 1851 |

QY 1798 GCAATGGGAGAGACCTGGAAATTTCTGGGGCAGCAGTGGAGCAGCCCGAGTGGGGG 1857  
DB 1852 GCAATGGGAGAGACCTGGAAATTTCTGGGGCAGCAGTGGAGCAGCCCGAGTGGGGG 1911  
QY 1858 GCCACCAAGTGGTCTTCCAGACAGATATCTCAGAGATGTFGFGAGGCACTGTCGAGC 1917  
DB 1912 GCCACCAAGTGGTCTTCCAGACAGATATCTCAGAGATGTFGFGAGGCACTGTCGAGC 1971  
QY 1918 GTTCTGCAATGGTCTGTCGTCAGCCCTGCTPACAAAGTGTACGTTGCTGTTTAAAAACA 1977  
DB 1972 GTTCTGCAATGGTCTGTCGTCAGCCCTGCTPACAAAGTGTACGTTGCTGTTTAAAAACA 2031  
QY 1978 TTGAGAGCCATGCTGGTATATCTCTTGCCACAGTTTGTAGCGGAAAGAAATCAAACTTCAG 2037  
DB 2032 TTGAGAGCCATGCTGGTATATCTCTTGCCACAGTTTGTAGCGGAAAGAAATCAAACTTCAG 2091  
QY 2038 AGACTTTCACAGCAGTGTAGACACCACTCTAGTCAAAATGTGCAGATGCCAATAGCCGC 2097  
DB 2092 AGACTTTCACAGCAGTGTAGACACCACTCTAGTCAAAATGTGCAGATGCCAATAGCCGC 2151  
QY 2098 ACAAGTCAGTGTCCATATCAACACTGTGTGAACCTGTGCAAGCCCAAGCAGAGAGTTG 2157  
DB 2152 ACAAGTCAGTGTCCATATCAACACTGTGTGAACCTGTGCAAGCCCAAGCAGAGAGTTG 2211  
QY 2158 GCAGTTGCAGAGAAATCTAAAGCTGGATCCATTTGGTATTTGGTGTGTTGATTATGTC 2217  
DB 2212 GCAGTTGCAGAGAAATCTAAAGCTGGATCCATTTGGTATTTGGTGTGTTGATTATGTC 2271  
QY 2218 TTAATTTGATTTCTTTGAAACCAAACTGAAATCAAACTGAAATTTGTCGCGC 2277  
DB 2272 TTAATTTGATTTCTTTGAAACCAAACTGAAATCAAACTGAAATTTGTCGCGC 2331  
QY 2278 CTTTGTCTATAGATAGACTGTGTGGAATTTCTGCTGAAATTTTATCCTCATATGTC 2337  
DB 2332 CTTTGTCTATAGATAGACTGTGTGGAATTTCTGCTGAAATTTTATCCTCATATGTC 2391  
QY 2338 AGTACTGATGTTTCAACAGCTGAGCCTGTGAAATCAGGTATAGAAAGCTGCTGTCCTC 2397  
DB 2392 AGTACTGATGTTTCAACAGCTGAGCCTGTGAAATCAGGTATAGAAAGCTGCTGTCCTC 2451  
QY 2398 TTAACCTTTGCTTTGCACTGATGATTAATTTCCCACTCAATGGTGGCAACCTTCCAGA 2457  
DB 2452 TTAACCTTTGCTTTGCACTGATGATTAATTTCCCACTCAATGGTGGCAACCTTCCAGA 2511  
QY 2458 AGGATCTACTTGAGTTCTGCAAGAAATGGTTACTACAGTACCCCATGTGTTTCAAAACTG 2517  
DB 2512 AGGATCTACTTGAGTTCTGCAAGAAATGGTTACTACAGTACCCCATGTGTTTCAAAACTG 2571  
QY 2518 TTAGAAATGCTGAGTGTTCAGTTCGACTCACTTACAGGATGCGTCGCCGTTTGATG 2577  
DB 2572 TTAGAAATGCTGAGTGTTCAGTTCGACTCACTTACAGGATGCGTCGCCGTTTGATG 2631  
QY 2578 GCTATTGCAGATGAGTGGAAATTTGCCGAAGCCATCCAGTTGGGCGTAGAAGACACTTTG 2637  
DB 2632 GCTATTGCAGATGAGTGGAAATTTGCCGAAGCCATCCAGTTGGGCGTAGAAGACACTTTG 2691  
QY 2638 GATGTCACAGGACAGCTTCTTGACGCACTGTGTTCCCAACAATCTATCTGGAACCCACA 2697  
DB 2692 GATGTCACAGGACAGCTTCTTGACGCACTGTGTTCCCAACAATCTATCTGGAACCCACA 2751  
QY 2698 GAGAACAGTTCCCTGAGTCACAGTCCATTTAGGAAACCTGGAAGAGGATATGCT 2757  
DB 2752 GAGAACAGTTCCCTGAGTCACAGTCCATTTAGGAAACCTGGAAGAGGATATGCT 2811  
QY 2758 ACAAATTTGAGTGCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGCATTTTCAGTAGGA 2817  
DB 2812 ACAAATTTGAGTGCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGCATTTTCAGTAGGA 2871  
QY 2818 CTTCTAGTTCAACACACACACACACACACACACACACACACACACACACACACACACAC 2877  
DB 2872 CTTCTAGTTCAACACACACACACACACACACACACACACACACACACACACACACACAC 2931

QY 2878 ACAAAGGAGAGACCCCAAGCTAGTGTGTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2937  
DB 2932 ACAAAGGAGAGACCCCAAGCTAGTGTGTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2991  
QY 2938 TTAATGTTTTCAGCCCTTGTCAACCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2997  
DB 2992 TTAATGTTTTCAGCCCTTGTCAACCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3051  
QY 2998 GCACACAGATGCTCTTAAGCATAGACTTCAGGGATTCATTCTCTGTCAGAAATACCTTCTGCA 3057  
DB 3052 GCACACAGATGCTCTTAAGCATAGACTTCAGGGATTCATTCTCTGTCAGAAATACCTTCTGCA 3111  
QY 3058 TCTCTCTAAACACAGCGGCAAGTTTCTCTCAATTCACAGAACTGCTCTGAAACAAA 3117  
DB 3112 TCTCTCTAAACACAGCGGCAAGTTTCTCTCAATTCACAGAACTGCTCTGAAACAAA 3171  
QY 3118 GACTCAGATAAACTTTCCCCAGTCTTACTCAGTCAAGACCTTCCCTCCAGATAACATA 3177  
DB 3172 GACTCAGATAAACTTTCCCCAGTCTTACTCAGTCAAGACCTTCCCTCCAGATAACATA 3231  
QY 3178 CACGCGCAAAAGCCATCTAGACCTTACCOCAGGTAAATACAAATAACAGGGAGATCCCTCA 3237  
DB 3232 CACGCGCAAAAGCCATCTCGACCTTACCCCAAGTAAATACAAATAACAGGGAGATCCCTCA 3291  
QY 3238 AAAAATAGCATGACACTTGTACTGAAACAGTAGTTCCAAATGTGATGACAGCTTTGGCTGT 3297  
DB 3292 AAAAATAGCATGACACTTGTACTGAAACAGTAGTTCCAAATGTGATGACAGCTTTGGCTGT 3351  
QY 3298 AGCAGCAATPAGTGTGTTATATCCAGTGCAGACAGTGTTCACCCAGTAGAG 3357  
DB 3352 AGCAGCAATPAGTGTGTTATATCCAGTGCAGACAGTGTTCACCCAGTAGAG 3411  
QY 3358 GAGAAATCAGATTAGATGTCATACAGAGCTCAACTCCAGTATTGAGAGACCTTCTTCAA 3417  
DB 3412 GAGAAATCAGATTAGATGTCATACAGAGCTCAACTCCAGTATTGAGAGACCTTCTTCAA 3471  
QY 3418 GCATCTATGCTTCAAGTGATAACAACAGTAACTTTTAAAGTCAGAGTTGCTGTCTGTCT 3477  
DB 3472 GCATCTATGCTTCAAGTGATAACAACAGTAACTTTTAAAGTCAGAGTTGCTGTCTGTCT 3531  
QY 3478 CTTGAAAGGCTGAAATGATGATACCTACAAAGATGATGTAATCATATAAATAAAGTGC 3537  
DB 3532 CTTGAAAGGCTGAAATGATGATACCTACAAAGATGATGTAATCATATAAATAAAGTGC 3591  
QY 3538 AAAGAGAGATGGAAGCTGAAGAGAGAAAGCTTTTGAACAATTCGCAATGCGCAATGTCAGCG 3597  
DB 3592 AAAGAGAGATGGAAGCTGAAGAGAGAAAGCTTTTGAACAATTCGCAATGTCAGCG 3651  
QY 3598 TCTCAGGATGCCCTCCCATAGTTCTCAGCTGCAGGTTGAAATGGAGAGATATCATC 3657  
DB 3652 TCTCAGGATGCCCTCCCATAGTTCTCAGCTGCAGGTTGAAATGGAGAGATATCATC 3711  
QY 3658 ATTATTCAACAGGATACACAGACTCTTACCAGGACATACCAAGCAACCAACCGTAT 3717  
DB 3712 ATTATTCAACAGGATACACAGACTCTTACCAGGACATACCAAGCAACCAACCGTAT 3771  
QY 3718 AGAAGAGACACTGAATGCTGAAAGCTCAACAGATAGCCCTTGGAGCAATTTCTTCTTGT 3777  
DB 3772 AGAAGAGACACTGAATGCTGAAAGCTCAACAGATAGCCCTTGGAGCAATTTCTTCTTGT 3831  
QY 3778 TATCAGGCTCAAGATGTTGGAACTGAACTTTAATGGCTTTAAACAGTGACTTATGTC 3837  
DB 3832 TATCAGGCTCAAGATGTTGGAACTGAACTTTAATGGCTTTAATACAGTGACTTATGTC 3891  
QY 3838 AGAAGACACTTCTTGAGCAAGAGATGATAGAGCACTAAGAGAGAGATAGATG 3897  
DB 3892 AGAAGACACTTCTTGAGCAAGAGATGATAGAGCACTAAGAGAGAGATAGATG 3951  
QY 3898 ATGAGCCATCTGAATCATCCAAACATATTAGGATGTTGGAGCCACCTGTTGAGAGAGC 3957  
DB 3952 ATGAGCCATCTGAATCATCCAAACATATTAGGATGTTGGAGCCACCTGTTGAGAGAGC 4011  
QY 3958 AATTACAATCTCTTCAATTGAATGGATGGCAGGGGATCGGTGGCTCATTTGCTGAGTAAA 4017

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Db 4012 AATTACATCTCTTCATTTGAATGATGCGAGGGGATCGTGGCTCATTTGCTGAGTAA 4071
Qy 4018 ATGAGAGCCTTCAAGAGATCAGTAGTTATTAACATCAGTGAACAGTTACTCGTGGCCTT 4077
Db 4072 ATGAGAGCCTTCAAGAGATCAGTAGTTATTAACATCAGTGAACAGTTACTCGTGGCCTT 4131
Qy 4078 TCGTATCTCCATGAAACCAATCATTTACAGAGATGTCAAAGGTGCCAAATTTGCTAATT 4137
Db 4132 TCGTATCTCCATGAAACCAATCATTTACAGAGATGTCAAAGGTGCCAAATTTGCTAATT 4191
Qy 4138 GACAGACTGTGTCAGAGACTAAGAAATGCAAGTTTGGAGCTGCGAGCCAGTGTGCATCA 4197
Db 4192 GACAGACTGTGTCAGAGACTAAGAAATGCAAGTTTGGAGCTGCGAGCCAGTGTGCATCA 4251
Qy 4198 AAGGAACTGTGTCAGAGAGTTTCAGGACAAATTTACTTGGGACAAATTTGCAATTTATGSCA 4257
Db 4252 AAGGAACTGTGTCAGAGAGTTTCAGGACAAATTTACTTGGGACAAATTTGCAATTTATGSCA 4311
Qy 4258 CCGAGGCTACTAAGAGGTCAACAGTATGGAAGGAGCTGTGATGTATGGAGTGTGGCTGT 4317
Db 4312 CCGAGGCTACTAAGAGGTCAACAGTATGGAAGGAGCTGTGATGTATGGAGTGTGGCTGT 4371
Qy 4318 GCTATTATAGAAATGCTTGTGCAAAACCAACATGGAATGCAAGAAACATCCCAATCAT 4377
Db 4372 GCTATTATAGAAATGCTTGTGCAAAACCAACATGGAATGCAAGAAACATCCCAATCAT 4431
Qy 4378 CTGCTTTGATATTTAAAGATTGCTAGTCAACTACTGCTCCATCGATCCCTTCAATTTG 4437
Db 4432 CTGCTTTGATATTTAAAGATTGCTAGTCAACTACTGCTCCATCGATCCCTTCAATTTG 4491
Qy 4438 TCTCCTGTTTACGAGATGCTCTTGTGTTTGTAGAACTTCAACCTCAGACAGACCT 4497
Db 4492 TCTCCTGTTTACGAGATGCTCTTGTGTTTGTAGAACTTCAACCTCAGACAGACCT 4551
Qy 4498 CCATCAAGAGAGCTACTGAAGCATCCAGTCCTTCTGACTACATGTGTAGCAATTTATGAG 4557
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Qy 4558 ATCACTACAGTAGAAGAGAGTGTCTCAACAGAGAAAGAACTTTGGGGAAACCAT 4617
Db 4612 ATCACTACAGTAGAAGAGAGTGTCTCAACAGAGAAAGAACTTTGGGGAAACCAT 4671
Qy 4618 TGATATTTCTACTGGCCATGATCCCATGCAAGCTATGAAAGAGCCAGTGGGAAACCT 4677
Db 4672 TGATATTTCTACTGGCCATGATCCCATGCAAGCTATGAAAGAGCCAGTGGGAAACCT 4731
Qy 4678 TACCTAAGTATGTGATTGCAAAATCATGATCTGTACCTAAGCTCAGTATGCAAAAGCCCA 4737
Db 4732 TACCTAAGTATGTGATTGCAAAATCATGATCTGTACCTAAGCTCAGTATGCAAAAGCCCA 4791
Qy 4738 AACTAGTGAGAACTGTAAACTGTGCTTTTCAAGAACTGGCCCTAGG 4786
Db 4792 AACTAGTGAGAACTGTAAACTGTGCTTTTCAAGAACTGGCCCTAGG 4840
```

## RESULT 3

```
AAFP27079
ID AAFP27079 standard; DNA; 4693 BP.
XX
AC AAFP27079;
XX
DT 06-APR-2001 (first entry)
XX
DE Human MEK1 cdna.
XX
KW Human MEK1; mitogen-activated protein kinase kinase kinase 1;
KW MEK kinase 1; MAP/ERK kinase kinase 1; pro-apoptotic;
KW apoptosis signal regulation; programmed cell death;
KW serine/threonine kinase; MAP kinase cascade; JNK/SAPK;
KW Jun N-terminal kinase/stress-activated protein kinase; Bcl-2 substrate;
KW NF-kappa-B-mediated transcription regulation; expression inhibition;
KW antisense therapy; hyperproliferative disorder; cancer; inflammation; ss.
```

```
XX Homo sapiens.
XX Key Location/Qualifiers
FT mat_peptide 1..4485
FT /*tag= a
FT /product= "Human MEK1"
XX
XX US6168950-B1.
XX
XX 02-JAN-2001.
XX
XX 23-JUL-1999; 99US-00359756.
XX
XX 23-JUL-1999; 99US-00359756.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Cowseert LM, Gaarde W, Ward DT;
XX
XX WPI; 2001-122264/13.
XX
XX P-PSDB; AAB60291.
XX
XX New antisense compound targeting nucleic acid encoding human mitogen-
XX activated protein kinase 1 (MEK1), useful for treating diseases
XX or conditions associated with MEK1 expression, or preventing
XX inflammation or tumor formation.
XX
XX Claim 1; Col 42-54; 35pp; English.
XX
XX This sequence represents human MEK1 cdna. MEK1 (also known as mitogen-
XX activated protein kinase kinase 1, MEK kinase 1 and MAP/ERK kinase
XX kinase 1) is a dual-specific serine/threonine kinase which mediates
XX cellular responses to mitogenic stimuli, being involved in JNK/SAPK (Jun
XX N-terminal kinase/stress-activated protein kinase) MAP kinase cascades.
XX MEK1 regulates signalling events associated with apoptosis (programmed
XX cell death) and NF-kappa-B, both of which have been associated with the
XX development of hyperproliferative disorders such as cancer. Specifically,
XX MEK1 lies directly downstream of Bcl-2 in an apoptotic signalling
XX cascade, and plays a critical role in the control of NF-kappa-B-mediated
XX transcription at multiple points in the apoptotic cascade. The invention
XX relates to antisense oligonucleotides targeted to the human MEK1 gene,
XX which inhibit its expression. A series of oligonucleotides (AAFP27086-
XX AAFP27125) were designed to target different regions of the human MEK1
XX RNA, and were analysed for their effect on MEK1 mRNA levels by
XX quantitative real-time PCR. The oligonucleotides of the invention are
XX useful for diagnosis, prevention and treatment of conditions associated
XX with MEK1 expression, such as inflammation, and cancer and other
XX hyperproliferative disorders
XX
XX Sequence 4693 BP; 1340 A; 1102 C; 1143 G; 1108 T; 0 U; 0 Other;
XX
XX Query Match 87.0%; Score 4564.6; DB 4; Length 4693;
XX Best Local Similarity 99.0%; Pred. No. 0;
XX Matches 4647; Conservative 0; Mismatches 39; Indels 9; Gaps 5;
XX
Qy 65 CGAGCCCTGAGGCGGCGGCGGAGGAGCCCTCAAGGCGAGCAGCGCCCGCGGCTG 124
Db 2 CGAGCCCTGAGGCGGCGGCGGAGGAGCCCTCAAGGCGAGCAGCGCGCGGCTG 61
Qy 125 CCGCGGAGCTGCTGCGGAGGCGGCGGAGCGCGGCGGCGGAGCGAGCTGCGCGGCGG 184
Db 62 CCGCGGAGCTGCTGCGGAGGCGGCGGAGCGCGGCGGCGGAGCTGCGCGGCGG 121
Qy 185 GGAGCTGCGCAAGTGCAGAGTGTGAGCTGACACAGCTGCTGTAGACCCCTCTTCC 244
Db 122 GGCAGCTGCGCAAGTGCAGAGTGTGAGCTGACACAGCTGCTGTAGACCCCTCTTCC 181
Qy 245 TTGCGGCTCACCGCGGCTCTCTCGACTTCCCGTGGCGGAGCCCGCGAGCGAGCGG 304
Db 182 TTGCGGCTCACCGCGGCTCTCTCGACTTCCCGTGGCGGAGCCCGCGAGCGAGCGG 241
Qy 305 GGAGTGGGACCGGCTCCACCTGTGGCGGTGCGCGCGCCGCCACGAGCGCGGCGG 364
```

Db 242 GGAGTGGGACCGGCTTCAGAGCTGTGGGGTGGCGGCCGCCACCGAGCCCGC 301  
Qy 365 GGGGCGCCACCTTACCAGAGTCGTGGGGGGCGCGGACAGCGGGCGCTCGAGTCCCGGAG 424  
Db 302 GGGGCGCCACCTTACCAGAGTCGTGGGGGGCGCGGACAGCGGGCGCTCGAGTCCCGGAG 361  
Qy 425 GGGGCGGACCGGGGAGAGCGGGCGCGCGCGCGCGCGCGCGCTCTCTGCGAGCGCGCGCG 484  
Db 362 GGGGCGGACCGGGGAGAGCGGGCGCGCGCGCGCGCGCGCGCTCTCTGCGAGCGCGCGCG 421  
Qy 485 CGGGTGGTGGAGTGGAGAAATAAGAAATCTCAAGGGTGGCAAGATGATGATGTC 544  
Db 422 CGGGTGGTGGAGTGGAGAAATAAGAAATCTCAAGGGTGGCAAGATGATGATGTC 481  
Qy 545 CAGAGGAACGAATGATCAGGAGAGAACTGAAGGCAACCTGTATGCGCAGCCTGGAGGACG 604  
Db 482 CAGAGGAACGAATGATCAGGAGAGAACTGAAGGCAACCTGTATGCGCAGCCTGGAGGACG 541  
Qy 605 AATGTTGGAAAGGAGAAATAGGCGAGGCGCTGTGGTAAACCAATCCCACTTAAAG 664  
Db 542 AATGTTGGAAAGGAGAAATAGGCGAGGCGCTGTGGTAAACCAATCCCACTTAAAG 601  
Qy 665 GAGATGGATCTGAATGAATCACTTAGCAGCTGAGTCTCCAGGAGAGTCCAGGCAAGTG 724  
Db 602 GAGATGGATCTGAATGAATCACTTAGCAGCTGAGTCTCCAGGAGAGTCCAGGCAAGTG 661  
Qy 725 CGGCTTCCAGCTTCCAAAGCCGACGAGCTCTCTCTGGCAACTCCCACTCAGGTC 784  
Db 662 CGGCTTCCAGCTTCCAAAGCCGACGAGCTCTCTCTGGCAACTCCCACTCAGGTC 721  
Qy 785 GCACAGTGAATCAGAACTCCAGAGTAGAGAGAAAGAGTTCCCACTGCTTTTC 844  
Db 722 GCACAGTGAATCAGAACTCCAGAGTAGAGAGAAAGAGTTCCCACTGCTTTTC 781  
Qy 845 AGAGTGGCAGAAATCACACCACCCGAGAGGCGCTTCCACAGAGTCTTCCACCATATA 904  
Db 782 AGAGTGGCAGAAATCACACCACCCGAGAGGCGCTTCCACAGAGTCTTCCACCATATA 841  
Qy 905 GCGCTGAGGAAACAAACCGCGTGTAAACAAAGTAGTGGGGCGAGCTGACTTACTGTC 964  
Db 842 GCGCTGAGGAAACAAACCGCGTGTAAACAAAGTAGTGGGGCGAGCTGACTTACTGTC 901  
Qy 965 AGCAGATAGGGGCTAACTCTTTCCTGATTGGAGGAGACAGCCAGACAAATAAACCGG 1024  
Db 902 AGCAGATAGGGGCTAACTCTTTCCTGATTGGAGGAGACAGCCAGACAAATAAACCGG 961  
Qy 1025 TGTATTGGGCGCTCAGAACTCAGAGTGTGACGTGGAAACATTCTGTAATCATCTGCTAT 1084  
Db 962 TGTATTGGGCGCTCAGAACTCAGAGTGTGACCATGGAACATTCTGTAATCATCTGCTAT 1021  
Qy 1085 TTGTGATGTCGGGGTGTTCAACTAGAACCTTCAGAACCCAAATGTTATGGAGAAACCTT 1144  
Db 1022 TTGTGATGTCGGGGTGTTCAACTAGAACCTTCAGAACCCAAATGTTATGGAGAAACCTT 1081  
Qy 1145 TAAAGAAATTTGAGGTTGAGATTTGTTCCAGAAATATCACAGTAGGCGTAGCTCAAGGA 1204  
Db 1082 TAAAGAAATTTGAGGTTGAGATTTGTTCCAGAAATATCACAGTAGGCGTAGCTCAAGGA 1141  
Qy 1205 TCAAGCTCCATCTCGTAAACCATCCAGAGTTTGTTCAGCATGTCAAATCTCATATA 1264  
Db 1142 TCAAGCTCCATCTCGTAAACCATCCAGAGTTTGTTCAGCATGTCAAATCTCATATA 1201  
Qy 1265 CATGTGTCATCTAGTACTTCTAGCTGTAGTTCAGAAACAGCATAAAGGATGAAGAGG 1324  
Db 1202 CATGTGTCATCTAGTACTTCTAGCTGTAGTTCAGAAACAGCATAAAGGATGAAGAGG 1261  
Qy 1325 AACAGATGTCCTATTCTGTTGGGCATCTGTGAAGAAAGTCTTACAGTGTGTCG 1384  
Db 1262 AACAGATGTCCTATTCTGTTGGGCATCTGTGAAGAAAGTCTTACAGTGTGTCG 1321  
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Db 1442 TCTACAGCCACAGAGTTGTCAAGTCTCTGGATTTCCCTTTCTTCCCTCAGAGTGCACAGC 1501  
Qy 1565 AGCAAAACCGTACAGCAGCAGCCTTTGGCTGGATCAAGAAAGATCAAGAGACCAATTTTA 1624  
Db 1502 AGCAAAACCGTACAGCAGCAGCCTTTGGCTGGATCAAGAAAGATCAAGAGACCAATTTTA 1561  
Qy 1625 ACCTTACTCATTTATGGAATCTCAGCAAAATCCCTCTCTGTACAAAGATTTAGCTGAGCCAT 1684  
Db 1562 ACCTTACTCATTTATGGAATCTCAGCAAAATCCCTCTCTGTACAAAGATTTAGCTGAGCCAT 1621  
Qy 1685 GHAATCAGTGTGTGAATGGAACTCGTTGGCTGCTTATTTCTTAGAAACTGGAATGTGA 1744  
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Db 1862 CAATGTGCTGTGCTGACCCCTGTCTACAAAGTGTAGTGTGCTGCTTTAAAAACATTGAGAG 1921  
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Qy 2165 GCAGAGAAATACATAAAGCTGGATCCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2224  
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Qy 2465 ACTTGAGTCTGCAAGATGTTTACTACAGTACCCCATGTTGTTTCCAAACTGTTAGAAA 2524  
Db 2402 ACTTGAGTCTGCAAGATGTTTACTACAGTACCCCATGTTGTTTCCAAACTGTTAGAAA 2461







Db 962 TGTTATTGGGCTCAGAACTGCAGCTGTGCACATGGACATTTCTGTATTTCATCTGCTAT 1021  
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Db 1022 TTGTGATGCTCGGGTGTTCACCTAGAACCTTCAGACCCAAATGTTATGGAGAAAACTT 1081  
Qy 1145 TAAAGAAATTTTTCAGAGTTGAGAGTTGTTTCCAGAAATATCAGTAGGCGTAGCTCAAGGA 1204  
Db 1082 TAAAGAAATTTTTCAGAGTTGAGAGTTGTTTCCAGAAATATCAGTAGGCGTAGCTCAAGGA 1141  
Qy 1205 TCAAGCTCCATCTCGTAACACATCAGAAATTTGTTTACGATGTCATTAATTCATTA 1264  
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Qy 1385 AAGACGGCTGCAGAAACAGCTGCACCACTCATGTCATTAATTTGGCGCAGAGAGTGA 1444  
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Qy 1445 GAAGAAATAGAAACCTTTAATATGTCCCTTTTGTAGATCTAAGTGGAGATCTCATGAT 1504  
Db 1382 GAAGAAATAGAAACCTTTAATATGTCCCTTTTGTAGATCTAAGTGGAGATCTCATGAT 1441  
Qy 1505 TCTACAGCTCAGAGTTGTCAGTCTGTCGATCCCTTCTTCCCTCAGAGCTGCACAGC 1564  
Db 1442 TCTACAGCTCAGAGTTGTCAGTCTGTCGATCCCTTCTTCCCTCAGAGCTGCACAGC 1501  
Qy 1565 AGCAAAACCTGACAGCAGCCTTTGGCTGATCAGAAAGAAATCAAGAGAGCAATTTTA 1624  
Db 1502 AGCAAAACCTGACAGCAGCCTTTGGCTGATCAGAAAGAAATCAAGAGAGCAATTTTA 1561  
Qy 1625 ACCTTACTCATATGGAATCAGCAATCCCTCTCTTCAAGATTTAGCTGAGCCAT 1684  
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Qy 1685 GGATTCAGGTGTTGGATGAAATCGTTGCTGCTTATTTCTAGAAACTGGAATGTGA 1744  
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Db 1982 TCCAGCCAGTTGTAGACACCATCTAGTCAATGTGCAGATGCCAATAGCGCAAGTC 2041  
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Qy 2165 GCAGAGAAATATCAAAAGCTGGAATCCATTTGGTATTGGTGGTGTGATTAATGCTTAAAT 2224  
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Qy 2225 GTATTCTTGGAAACCAAACTGAATCAAACTGAATCAAACTGAATCAAACTGAATCAAACT 2284  
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Db 2222 TTATAGATAGACTGTTGTTGGAAATTTCTGCTGAATTTTATCTCATATTTGTCAGTACTG 2281  
Qy 2345 ATGTTTCAACAGCTGAGCGCTGTTGAAATCAAGATATAAGAGCTGCTGCTCTTAACT 2404  
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Qy 2405 TTGCTTTGCACTGCTAATGATTAATCCCACTCAATGTTGGCAAACTTTCCAGAAAGATCT 2464  
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Qy 2525 TGTGAGTGTTCCTAG--TTCCACTCACTTCCAGGATGCTGCTGCGCTTTGATGGCTA 2581  
Db 2462 TGTGAGTGTTCCTAGTGTTCCTCACTTCCAGGATGCTGCTGCGCTTTGATGGCT 2521  
Qy 2582 TTGCGATGAGTGGAAATGCGGAGCCATCCAGTTGGGCGTAGAAGACACTTTGGATG 2641  
Db 2522 ATGCGATGAGTGGAAATGCGGAGCCATCCAGTTGGGCGTAGAAGACACTTTACAAC 2581  
Qy 2642 GTCAACAGGACAGC--TTCTTGCAGGCTATCTGTTCCCACTACTATCTGGAACACACAGA 2699  
Db 2582 GACAAACACACACAGCTTTTGCAGGCTATCTGTTCCCACTACTATCTGGAACACACAGA 2641  
Qy 2700 GAACAGTTCCTC--TGAGTGCAAGTCCATTTAGAGAAACTGGAAGAGATATGCTA 2758  
Db 2642 GAACAGTTCCTCCTTGAAGTGCAAGTCCATTTAGAGAAACTGGAAGAGATATGCTA 2701  
Qy 2759 CAAAATTTAGTGCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGCAATTTCAAGTAGGAC 2818  
Db 2702 CAAAATTTAGTGCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGCAATTTCAAGTAGGAC 2761  
Qy 2819 CTTCTAGTTCAACACACACACACACACACACACACACACACACACACACACACACAC 2878  
Db 2762 CTTCTAGTTCAACACACACACACACACACACACACACACACACACACACACACAC 2821  
Qy 2879 CAAAAGGACAGCCACAGTCAAGTGTGAACTCTCTCTCTTATCTCATATCCCAAT 2938  
Db 2822 CAAAAGGACAGCCACAGTCAAGTGTGAACTCTCTCTCTTATCTCATATCCCAAT 2881  
Qy 2939 TAATGTTTCCAGCTGTCAACCCCTTCTTCTTCTTACCCCATCTGTACAGCTGGCAGT 2998  
Db 2882 TAATGTTTCCAGCTGTCAACCCCTTCTTCTTCTTACCCCATCTGTACAGCTGGCAGT 2941  
Qy 2999 CAAAGATGCTCTTAAGCATAGACTTCAAGGATTTCAATCCCTGCGAGATACCTTCTGAT 3058  
Db 2942 CAAAGATGCTCTTAAGCATAGACTTCAAGGATTTCAATCCCTGCGAGATACCTTCTGAT 3001  
Qy 3059 CTCCTCAACACAGCGCAAGTTTCTCTCAATTTCCAGAACTGTCTCTGAAAAAAG 3118  
Db 3002 CTCCTCAACACAGCGCAAGTTTCTCTCAATTTCCAGAACTGTCTCTGAAAAAAG 3061  
Qy 3119 ACTCAGATAACTTTCCCGCTTTTACTCAGTCAAGACCTTGGCCCTCCAGTACATAC 3178  
Db 3062 ACTCAGATAACTTTCCCGCTTTTACTCAGTCAAGACCTTGGCCCTCCAGTACATAC 3121  
Qy 3179 ACAGGCCAAAGCCATCTAGACCTACCCAGGTAATACAAAGTAAACAGGAGATCCCTCAA 3238  
Db 3122 ACAGGCCAAAGCCATCTAGACCTACCCAGGTAATACAAAGTAAACAGGAGATCCCTCAA 3181

|    |      |                                                                          |      |
|----|------|--------------------------------------------------------------------------|------|
| Qy | 3239 | AAAATGACATGACACATTGATCTCGAACACGATGATGTCCTCCAAATGTGTGATGACACGCTTTGGCTGTAT | 3298 |
| Db | 3182 | AAAATGACATGACACATTGATCTCGAACACGATGATGTCCTCCAAATGTGTGATGACACGCTTTGGCTGTGA | 3241 |
| Qy | 3299 | GCAGCAATAGTAGTAATGCTGTTATATACCCAGTCACGAGACAGTGTGTTACCCACAGTAGAGG         | 3358 |
| Db | 3242 | GCAGCAATAGTAGTAATGCTGTTATATACCCAGTCACGAGACAGTGTGTTACCCACAGTAGAGG         | 3301 |
| Qy | 3359 | AGAAATGCAGATTAGATGTCAATACAGAGCTCAACTCCAGTATTTGAGGACCTTCTTTGAAG           | 3418 |
| Db | 3302 | AGAAATGCAGATTAGATGTCAATACAGAGCTCAACTCCAGTATTTGAGGACCTTCTTTGAAG           | 3361 |
| Qy | 3419 | CATCTATGCGCTTCAAGTGATACAAACAGTAACTTTTAAAGTCAGAAGTGTGCTGCTGCTCTC          | 3478 |
| Db | 3362 | CATCTATGCGCTTCAAGTGATACAAACAGTAACTTTTAAAGTCAGAAGTGTGCTGCTGCTCTC          | 3421 |
| Qy | 3479 | CTGGAAGGCTGGAATGATGATACCTTACAAAGATGATGTGATCATATATCAAAAGTGCA              | 3538 |
| Db | 3422 | CTGGAAGGCTGGAATGATGATACCTTACAAAGATGATGTGATCATATATCAAAAGTGCA              | 3481 |
| Qy | 3539 | AAGAGAAGATGGAAGCTGGAAGAAGAAAGCTTTTAGCAATTTGCCATGTCCAGCGT                 | 3598 |
| Db | 3482 | AAGAGAAGATGGAAGCTGGAAGAAGAAAGCTTTTAGCAATTTGCCATGTCCAGCGT                 | 3541 |
| Qy | 3599 | CTCAGGATGCCCTCCCATAGTTTCTTCAGCTGCAGCTGGAATTTGAAATGAGAGATATCATCA          | 3658 |
| Db | 3542 | CTCAGGATGCCCTCCCATAGTTTCTTCAGCTGCAGCTGGAATTTGAAATGAGAGATATCATCA          | 3601 |
| Qy | 3659 | TTATTTCAACAGGATPACCCAGAGACTCTACCCAGGACATACCAAAGCAAAACCAACCGTATA          | 3718 |
| Db | 3602 | TTATTTCAACAGGATPACCCAGAGACTCTACCCAGGACATACCAAAGCAAAACCAACCGTATA          | 3661 |
| Qy | 3719 | GAGAAGACACTGGAATGCTCGAAAGGTCACACAGATAGGCCCTTGAGACATTTTCTTCTTGTT          | 3778 |
| Db | 3662 | GAGAAGACACTGGAATGCTCGAAAGGTCACACAGATAGGCCCTTGAGACATTTTCTTCTTGTT          | 3721 |
| Qy | 3779 | ATCAGGCTCAAGATGTGGGAACCTGGAACCTTTAATGGCTGTATAACAGGTGACTTTATGTCA          | 3838 |
| Db | 3722 | ATCAGGCTCAAGATGTGGGAACCTGGAACCTTTAATGGCTGTATAACAGGTGACTTTATGTCA          | 3781 |
| Qy | 3839 | GAAACACATCTTCTGACCAAGAGAAGTAGTAGAAGCACATAAGAGAAGAGATAGAATGA              | 3898 |
| Db | 3782 | GAAACACATCTTCTGACCAAGAGAAGTAGTAGAAGCACATAAGAGAAGAGATAGAATGA              | 3841 |
| Qy | 3899 | TGAGCCATCTGAATCATCCAAAACATATTAGGATGTTGGAGGCCACGTTGGAAGAGCA               | 3958 |
| Db | 3842 | TGAGCCATCTGAATCATCCAAAACATATTAGGATGTTGGAGGCCACGTTGGAAGAGCA               | 3901 |
| Qy | 3959 | ATTACAATCTCTTCATTGAAATGGATGCGAGGGGATCGGTGGCTCATTTTCTCAGTAAAT             | 4018 |
| Db | 3902 | ATTACAATCTCTTCATTGAAATGGATGCGAGGGGATCGGTGGCTCATTTTCTCAGTAAAT             | 3961 |
| Qy | 4019 | ATGAGGCTTCAAGAAATCAGTAGTTATTAACTACACTGAAACAGTTACTCCGTGGCGCTTT            | 4078 |
| Db | 3962 | ATGAGGCTTCAAGAAATCAGTAGTTATTAACTACACTGAAACAGTTACTCCGTGGCGCTTT            | 4021 |
| Qy | 4079 | CGTATCTCCATGAAAACCAAATCAATCACAGAGATGTCAAAGGTGCCAATTTTGTCTAATTG           | 4138 |
| Db | 4022 | CGTATCTCCATGAAAACCAAATCAATCACAGAGATGTCAAAGGTGCCAATTTTGTCTAATTG           | 4081 |
| Qy | 4139 | ACAGCACTGGTCAGAGACTAAGAATTCGAGATTTTGGAGCTGCAGCCAGCGTTGGCATCAA            | 4198 |
| Db | 4082 | ACAGCACTGGTCAGAGACTAAGAATTCGAGATTTTGGAGCTGCAGCCAGCGTTGGCATCAA            | 4141 |
| Qy | 4199 | AAGGAACCTGGTGCAGGAGGTTTCAGGGAACAATTTACTGGGGAACAATTTGCAATTTATGGCAC        | 4258 |
| Db | 4142 | AAGGAACCTGGTGCAGGAGGTTTCAGGGAACAATTTACTGGGGAACAATTTATGGCAC               | 4201 |
| Qy | 4259 | CTGAGGTACTAAGAGGTCACACAGTATGGAAGGACCTGTGATGTATGAGTGTGGCTGTG              | 4318 |
| Db | 4202 | CTGAGGTACTAAGAGGTCACACAGTATGGAAGGACCTGTGATGTATGAGTGTGGCTGTG              | 4361 |
| Qy | 4319 | CTATTATAGAAATGGCTTGTGCAAAAACCCATCATGGAATGCAGAAAAACACTCCCAATCATC          | 4378 |

## RESULT 5

|                                                                           |                         |
|---------------------------------------------------------------------------|-------------------------|
| AA588564                                                                  | standard; cDNA; 488 BP. |
| AA588564                                                                  |                         |
| AA568564                                                                  |                         |
| 13-FEB-2002                                                               | (first entry)           |
| DNA encoding novel human diagnostic protein #4368.                        |                         |
| Human; chromosome mapping; gene mapping; gene therapy; forensic;          |                         |
| food supplement; medical imaging; diagnostic; genetic disorder; ss.       |                         |
| Homo sapiens.                                                             |                         |
| WO200175067-A2.                                                           |                         |
| 11-OCT-2001.                                                              |                         |
| 30-MAR-2001; 2001WO-US008631.                                             |                         |
| 31-MAR-2000; 2000US-00540217.                                             |                         |
| 23-AUG-2000; 2000US-00649167.                                             |                         |
| (HYSE-) HYSEQ INC.                                                        |                         |
| Dmanac RT, Liu C, Tang YT;                                                |                         |
| WPI; 2001-639362/73.                                                      |                         |
| P-PSDB; ABG04377.                                                         |                         |
| New isolated polynucleotide and encoded polypeptides, useful in           |                         |
| diagnostics, forensics, gene mapping, identification of mutations         |                         |
| responsible for genetic disorders or other traits and to assess           |                         |
| biodiversity.                                                             |                         |
| Claim 1; SEQ ID NO 4368; 103pp; English.                                  |                         |
| The invention relates to isolated polynucleotide (I) and polypeptide (II) |                         |
| sequences. (I) is useful as hybridisation probes, polymerase chain        |                         |
| reaction (PCR) primers, oligomers, and for chromosome and gene mapping,   |                         |
|                                                                           |                         |

CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIFO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 4488 BP; 1264 A; 1057 C; 1101 G; 1066 T; 0 U; 0 Other;

Query Match 83.7%; Score 4390.6; DB 5; Length 4488;  
 Best Local Similarity 99.1%; Pred. No. 0;  
 Matches 4447; Conservative 0; Mismatches 34; Indels 6; Gaps 3;

QY 65 CGAGCCCTGAGGCGGCGGCGGAGAGCCCTCAAGCGAGCAGCGGCCCGGGCTG 124  
 DB 2 CGAGCCCTGAGGCGGCGGCGGAGAGCCCTCAAGCGAGCAGCGGCCCGGGCTG 61

QY 125 CCGCGGACTGCTCGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGG 184  
 DB 62 CCGCGGACTGCTCGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGG 121

QY 185 GGCAGCTGCGCAAGTGCAGAGTGTGTGAGCTGTGACCAAGCTGCTGAGCAGCGCTCTTCC 244  
 DB 122 GGCAGCTGCGCAAGTGCAGAGTGTGTGAGCTGTGACCAAGCTGCTGAGCAGCGCTCTTCC 181

QY 245 TTGCGCGCTCACCGCGGCTCTCTGACTTCCCGCTGCGCGGAGCGGCGGAGCGGCGG 304  
 DB 182 TTGCGCGCTCACCGCGGCTCTCTGACTTCCCGCTGCGCGGAGCGGCGGAGCGGCGG 241

QY 305 GAGTGGGAGCGGCTTCCAGCTGTGGCGGTGCGCGGCGGCGGCGGCGGCGGCGGCGG 364  
 DB 242 GAGTGGGAGCGGCTTCCAGCTGTGGCGGTGCGCGGCGGCGGCGGCGGCGGCGGCGG 301

QY 365 GCGGCGGCCACCTTACCGAGTGGTGGCGGCGGCGGAGCAGCGGCGCTGAGTCCCGAG 424  
 DB 302 GCGGCGGCCACCTTACCGAGTGGTGGCGGCGGCGGAGCAGCGGCGCTGAGTCCCGAG 361

QY 425 CCGCGAGCGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 484  
 DB 362 CCGCGAGCGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 421

QY 485 CCGGTCTGTGAGTGGAGAAATAAGAACTCTCAAGGGTTGCAAGAGTGGATGATCGTC 544  
 DB 422 CCGGTCTGTGAGTGGAGAAATAAGAACTCTCAAGGGTTGCAAGAGTGGATGATCGTC 481

QY 545 CAGAGGAGCAATGATCAGGAGAGAACTGAAGGCAACCTGTATGCCAGCTGGAAGCAGC 604  
 DB 482 CAGAGGAGCAATGATCAGGAGAGAACTGAAGGCAACCTGTATGCCAGCTGGAAGCAGC 541

QY 605 AATGGTTGGAAGAGAGAAATAGCGGCGGCTGTGGTGGTAAACCAATCCCAAGTTAAAG 664  
 DB 542 AATGGTTGGAAGAGAGAAATAGCGGCGGCTGTGGTGGTAAACCAATCCCAAGTTAAAG 601

QY 665 GAGATGATCTGAATGAACTAGACGTGAGTCTCCAGGAGGAGGTCAGGCGAGGTG 724  
 DB 602 GAGATGATCTGAATGAACTAGACGTGAGTCTCCAGGAGGAGGTCAGGCGAGGTG 661

QY 725 CCGCTTCCACAGCTTCCAAAGCGGAGCGAGTCTCTCTCTGGCAATCCCAATCAGGTC 784  
 DB 662 CCGCTTCCACAGCTTCCAAAGCGGAGCGAGTCTCTCTCTGGCAATCCCAATCAGGTC 721

QY 785 GCACAGTGAATCAGAACTCCAGAGTAAGGAGAAAGAGTTTCCCAAGTCCCTTTTC 844  
 DB 722 GCACAGTGAATCAGAACTCCAGAGTAAGGAGAAAGAGTTTCCCAAGTCCCTTTTC 781

QY 845 AGAGTGCAGAAATCACACACCCCGAGAGCCCTTCCACAGATGGCTTCTCAACCATATA 904  
 DB 782 AGAGTGCAGAAATCACACACCCCGAGAGCCCTTCCACAGATGGCTTCTCAACCATATA 841

QY 905 GCCCTGAGGAAACAAACCGCGGTGTTAAAGATGATGCGGCGCAGACTGTACTTCTGC 964  
 DB 842 GCCCTGAGGAAACAAACCGCGGTGTTAAAGATGATGCGGCGCAGACTGTACTTCTGC 901

QY 965 AGCAGATAGGCGCTAACTCTTCTGATTCGAGAGAGACGCCAGACAAATAAATACCGGG 1024  
 DB 902 AGCAGATAGGCGCTAACTCTTCTGATTCGAGAGAGACGCCAGACAAATAAATACCGGG 961

QY 1025 TGTATTATGGGCTCAGAACTGAGCTGTCAGTGGAAACATCTCTGATTCTATCTGCTAT 1084  
 DB 962 TGTATTATGGGCTCAGAACTGAGCTGTCAGTGGAAACATCTCTGATTCTATCTGCTAT 1021

QY 1085 TTGTGATGCTCCGGGTGTTTCAACTAGAACCTTCAGACCCCAATGTTATGAGAGAAAACCTT 1144  
 DB 1022 TTGTGATGCTCCGGGTGTTTCAACTAGAACCTTCAGACCCCAATGTTATGAGAGAAAACCTT 1081

QY 1145 TAAAGAAATTTGAGGTTGAGAGTTTGTTCAGAAATATCACAGTACGCTAGCTCAAGGA 1204  
 DB 1082 TAAAGAAATTTGAGGTTGAGAGTTTGTTCAGAAATATCACAGTACGCTAGCTCAAGGA 1141

QY 1205 TCAAAGTCCCATCTCTGTAACACCACTCCAGAGTTTGTTCACGATGTCATAAATCTCTATA 1264  
 DB 1142 TCAAAGTCCCATCTCTGTAACACCACTCCAGAGTTTGTTCACGATGTCATAAATCTCTATA 1201

QY 1265 CATGTGCATCATCTAGTACTTCTACATCTAGTTCAGAAAACAGCATAAAGATGAAGGG 1324  
 DB 1202 CATGTGCATCATCTAGTACTTCTACATCTAGTTCAGAAAACAGCATAAAGATGAAGGG 1261

QY 1325 AACAGATGTCCTATTGTTGTCGATGTTGATGAAGAAAGTCTTACAGTGTGTG 1384  
 DB 1262 AACAGATGTCCTATTGTTGTCGATGTTGATGAAGAAAGTCTTACAGTGTGTG 1321

QY 1385 AAGACGGCTGAGGAAACAAAGCTGCAACCACTGCTCAATTTGGGCGAAGAGTGTGA 1444  
 DB 1322 AAGACGGCTGAGGAAACAAAGCTGCAACCACTGCTCAATTTGGGCGAAGAGTGTGA 1381

QY 1445 GAAGAAATAGAGAACCTTTAATATGTCCTTCTGATCTAAGTGGAGATCTCATGATT 1504  
 DB 1382 GAAGAAATAGAGAACCTTTAATATGTCCTTCTGATCTAAGTGGAGATCTCATGATT 1441

QY 1505 TCTACAGCCACGAGTGTCAAGTCTGTGGATTCCCTTCTTCCCTCAGAGCTGCACAGC 1564  
 DB 1442 TCTACAGCCACGAGTGTCAAGTCTGTGGATTCCCTTCTTCCCTCAGAGCTGCACAGC 1501

QY 1565 AGCAACCGTACAGCGAGCGCTTTGGTGGATCAGAGGAATCAAGAGAGCAATTTTA 1624  
 DB 1502 AGCAACCGTACAGCGAGCGCTTTGGTGGATCAGAGGAATCAAGAGAGCAATTTTA 1561

QY 1625 ACCTTACTCATTTAGAACTCAGCAAAATCCCTCTGCTTACAAAGATTTAGTGGCCAT 1684  
 DB 1562 ACCTTACTCATTTAGAACTCAGCAAAATCCCTCTGCTTACAAAGATTTAGTGGCCAT 1621

QY 1685 GGAATCAGTGTGGAAATGGAATCTGTTGGCTCTTATTTCTAGAACTGGATGGA 1744  
 DB 1622 GGAATCAGTGTGGAAATGGAATCTGTTGGCTCTTATTTCTAGAACTGGATGGA 1681

QY 1745 GAGAGATGGCCCTCAGGCGTCTTTCCCATGATGTGAGTGGGCGCTGTCTTGGCAATG 1804  
 DB 1682 GAGAGATGGCCCTCAGGCGTCTTTCCCATGATGTGAGTGGGCGCTGTCTTGGCAATG 1741

QY 1805 GGGAGAGCACTGGAAATTTCTGGGGGAGCAGTGGAGAGCGGCGGAGTGGGGAGCCACA 1864  
 DB 1742 GGGAGAGCACTGGAAATTTCTGGGGGAGCAGTGGAGAGCGGCGGAGTGGGGAGCCACA 1801

QY 1865 GTGGGTCTTCCAGAGCCAGTATCTCAGGAGATGTGGTGGAGGATGCTGTCAGCGTCTGTG 1924

Db 1802 GTGGGCTTCCAGACAGTATCTCAGGAGATGTGTGGAGCATGTCTCAGCGTTCTGT 1861  
Qy 1925 CAATGGTCTGTGTGACCCCTGTCTACAAAGTGTACGTTGCTGCTTTAAAAAATTGAGAG 1984  
Db 1862 CAATGGTCTGTGTGACCCCTGTCTACAAAGTGTACGTTGCTGCTTTAAAAAATTGAGAG 1921  
Qy 1985 CCATGCTGTGTATATACTCCCTGTCACAGAGTTAGCGGAAAGAAATCAAACCTTCAGAGACTTC 2044  
Db 1922 CCATGCTGTGTATATACTCCCTGTCACAGAGTTAGCGGAAAGAAATCAAACCTTCAGAGACTTC 1981  
Qy 2045 TCCAGCCAGTTGTAGACACCATCTGTAGTCAAAATGTGAGAGTGCATAGCCGACAGATC 2104  
Db 1982 TCCAGCCAGTTGTAGACACCATCTGTAGTCAAAATGTGAGAGTGCATAGCCGACAGATC 2041  
Qy 2105 AGCTGTCCATATCAACACTGTTGGAACTGTGCAAGCCCAAGCAGGAGAGTTGGCAGTTG 2164  
Db 2042 AGCTGTCCATATCAACACTGTTGGAACTGTGCAAGCCCAAGCAGGAGAGTTGGCAGTTG 2101  
Qy 2165 GCAGAGAAATACATAAAGCTGGATCCATTTGGTATTTGGTGTGTGATTAAGTCTTAAT 2224  
Db 2102 GCAGAGAAATACATAAAGCTGGATCCATTTGGTATTTGGTGTGTGATTAAGTCTTAAT 2161  
Qy 2225 GTATTTCTGGAAACCAAACTGAATCAAAATTTGGCAAGAACTTTCTGGCCGCTTTGTC 2284  
Db 2162 GTATTTCTGGAAACCAAACTGAATCAAAATTTGGCAAGAACTTTCTGGCCGCTTTGTC 2221  
Qy 2285 TTATAGATAGACTGTTGTGAAATTTCCCTGCTGAATTTTATCCTCATATTTGTGAGTACTG 2344  
Db 2222 TTATAGATAGACTGTTGTGAAATTTCCCTGCTGAATTTTATCCTCATATTTGTGAGTACTG 2281  
Qy 2345 ATGTTTCAAGCTGAGCTGTTCAAAATCAGGTATAGAGAGTCTGCTCCCTCTTAACCT 2404  
Db 2282 ATGTTTCAAGCTGAGCTGTTGAATCAGGTATAGAGAGTCTGCTCCCTCTTAACCT 2341  
Qy 2405 TTGCTTTGAGTCCATTTGATTAATTTCCCACTCAATGTTGTCGAACTTTCCAGAGGATCT 2464  
Db 2342 TTGCTTTGAGTCCATTTGATTAATTTCCCACTCAATGTTGTCGAACTTTCCAGAGGATCT 2401  
Qy 2465 ACTTGAGTTCTGCAAGATGTTACTACAGTACCCCATGTTTCAAACTGTTAGAAA 2524  
Db 2402 ACTTGAGTTCTGCAAGATGTTACTACAGTACCCCATGTTTCAAACTGTTAGAAA 2461  
Qy 2525 TGCTGAGTGTTCAG--TTTCTTGCAGGCATCTGTTCCCAACTATCTGGAACCCACAGA 2581  
Db 2462 TGCTGAGTGTTCAGTGTGTTTCCACTCACTTCCAGGATGCGTGGCGTTGATGGCTT 2521  
Qy 2582 TTGCAGATGAGTGTGAAATTTCCGAGCCATCCAGTGGCGGTAGAGACACTTTGATG 2641  
Db 2522 ATGCAGATGAGTGTGAAATTTCCGAGCCATCCAGTGGCGGTAGAGACACTTTACAC 2581  
Qy 2642 GTCAACAGGACAGC--TTTCTTGCAGGCATCTGTTCCCAACTATCTGGAACCCACAGA 2699  
Db 2582 GACACACACACACAGCTTTTGCAGGCATCTGTTCCCAACTATCTGGAACCCACAGA 2641  
Qy 2700 GAACAGTGTCCCT--TGAGTGCACAGTCCATTTAGAGAACTGGAAGGATTTGCTTA 2758  
Db 2642 GAACAGTGTCCCTTTGAGTGCACAGTCCATTTAGAGAACTGGAAGGATTTGCTTA 2701  
Qy 2759 CAAAATTCAGTGTCCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGCACTTTCACTAGGAC 2818  
Db 2702 CAAAATTCAGTGTCCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGGATTTCACTAGGAC 2761  
Qy 2819 CTTCTAGTTTCAACACACACACACACACACACACACACACACACACACACACACACAC 2878  
Db 2762 CTTCTAGTTTCAACACACACACACACACACACACACACACACACACACACACACACAC 2821  
Qy 2879 CAAAAGGACAGCCACAGTGTGTTGAACTCCCTCTTATCTCATCATTTCCCAAT 2938  
Db 2822 CAAAAGGACAGCCACAGTGTGTTGAACTCCCTCTTATCTCATCATTTCCCAAT 2881  
Qy 2939 TAATGTTTCCAGCTGTGTCACACCCCTCTTCTTCTTACCCCATCTGTGTACAGCTGGACCTG 2998

Db 2882 TAATGTTTCCAGCTGTGTCACACCCCTTTCTTTCTATCCCATCTGTATCCAGCTGGCACTG 2941  
Qy 2999 CACAGATGTCTCTTAAGCATAGACTTCAGGGATTCATTTCCCTGAGAAATACCTTTCTGCAT 3058  
Db 2942 CACAGATGTCTCTTAAGCATAGACTTCAGGGATTCATTTCCCTGAGAAATACCTTTCTGCAT 3001  
Qy 3059 CTCCTCAAAACACAGCGGAAAGTTTCTCTACAAATTCACAGAAACTGTCTGAAAACAAAG 3118  
Db 3002 CTCCTCAAAACACAGCGGAAAGTTTCTCTACAAATTCACAGAAACTGTCTGAAAACAAAG 3061  
Qy 3119 ACTCAGATAAACTTTTCCCTCAGTCTTTACTCAGTCAAGACCCCTTGGCCCTCCAGTAACATAC 3178  
Db 3062 ACTCAGATAAACTTTTCCCTCAGTCTTTACTCAGTCAAGACCCCTTGGCCCTCCAGTAACATAC 3121  
Qy 3179 ACAGCCAAAGCCATCTAGACCTACCCAGGTAAATAAAGTAAACAGGGAGATCCCTCAA 3238  
Db 3122 ACAGCCAAAGCCATCTCGACCTACCCAGGTAAATAAAGTAAACAGGGAGATCCCTCAA 3181  
Qy 3239 AAAATAGCATCACACTTTGATCTGAAACAGTAGTTCCAAATGTGATGACAGCTTTGGCTGTA 3298  
Db 3182 AAAATAGCATCACACTTTGATCTGAAACAGTAGTTCCAAATGTGATGACAGCTTTGGCTGTA 3241  
Qy 3299 GCAGCAATAGTAGTAATGTCTTTATACCCAGTGCAGAGACAGTGTTCACCCAGTAGAGG 3358  
Db 3242 GCAGCAATAGTAGTAATGTCTTTATACCAAGTGCAGAGACAGTGTTCACCCAGTAGAGG 3301  
Qy 3359 AGAATGACAGATTAGATGTCAATACAGAGCTCAACTCCAGTATTTAGAGACCTTTCTTGAAG 3418  
Db 3302 AGAATGACAGATTAGATGTCAATACAGAGCTCAACTCCAGTATTTAGAGACCTTTCTTGAAG 3361  
Qy 3419 CATCTATCCCTTCAAGTGATACAAACAGTAACTTTTAAAGTCAAGAGTGTCTGCTGCTC 3478  
Db 3362 CATCTATCCCTTCAAGTGATACAAACAGTAACTTTTAAAGTCAAGAGTGTCTGCTGCTC 3421  
Qy 3479 CTGAAAGGCTCAAAATGATGATCTCAAAAGATGATGCAATCATATCAAAAGTGCA 3538  
Db 3422 CTGAAAGGCTCAAAATGATGATCTCAAAAGATGATGCAATCATATCAAAAGTGCA 3481  
Qy 3539 AAGAGAAGATGGAAGCTCAAGAGAGAGCTTTAGCAATTTGCCATGCGCAATGTGCGGT 3598  
Db 3482 AAGAGAAGATGGAAGCTCAAGAGAGAGAGCTTTAGCAATTTGCCATGCGCAATGTGCGGT 3541  
Qy 3599 CTCAGATGCTCCCTCCCTCAGTGTCTCAGTGCAGGTTGAAAATGGAGAGATATCATCA 3658  
Db 3542 CTCAGTGTCCCTCCCTCAGTGTCTCAGTGCAGGTTGAAAATGGAGAGATATCATCA 3601  
Qy 3659 TTATTCACACAGGATACACAGAGACTCTACAGAGACATCCAAAGCAAAAACACCGTATA 3718  
Db 3602 TTATTCACACAGGATACACAGAGACTCTACAGAGACATCCAAAGCAAAAACACCGTATA 3661  
Qy 3719 GAGAGACACTGAATGGCTGAAAGGTCAACAGATAGGCTTTGGAGCATTTTCTTCTGTT 3778  
Db 3662 GAGAGACACTGAATGGCTGAAAGGTCAACAGATAGGCTTTGGAGCATTTTCTTCTGTT 3721  
Qy 3779 ATCAGGCTCAAGATGTGGGAACTGGAACTTTAATGGCTTTTAAACAGGTGATATGCA 3838  
Db 3722 ATCAGGCTCAAGATGTGGGAACTGGAACTTTAATGGCTTTTAAACAGGTGATATGCA 3781  
Qy 3839 GAAACACATCTTCTGAGCAAGAGAGTAGTAGAGCACTAAGAGAGAGATAGAAATGA 3898  
Db 3782 GAAACACATCTTCTGAGCAAGAGAGTAGTAGAGCACTAAGAGAGAGATAGAAATGA 3841  
Qy 3899 TGAGCCATCTGAATCATCCAAACATCATTTAGGATGTGGGAGCCACGTTGTGAGAGAGCA 3958  
Db 3842 TGAGCCATCTGAATCATCCAAACATCATTTAGGATGTGGGAGCCACGTTGTGAGAGAGCA 3901  
Qy 3959 ATTACAACTCTTCTGAATGAGTGGAGGGGATCGGTGCTCATTTGCTGAGTAAT 4018  
Db 3902 ATTACAACTCTTCTGAATGAGTGGAGGGGATCGGTGCTCATTTGCTGAGTAAT 3961  
Qy 4019 ATGAGCCTTCAAGAAATCAGTAGTTAATTAATCACTGAACAGATTACTCCCTGGCCTTT 4078  
Db 3962 ATGAGCCTTCAAGAAATCAGTAGTTAATTAATCACTGAACAGATTACTCCCTGGCCTTT 4021

QY 4079 CGTATCTCCATGAAAAACAAATCAATTCACAGAGATGTCAAAGGTGCCAATTTGCTAATTG 4138  
Db 4022 CGTATCTCCATGAAAAACAAATCAATTCACAGAGATGTCAAAGGTGCCAATTTGCTAATTG 4081  
QY 4139 ACAGCACTGGTCAGAGACTAAGAAATTCAGATTTTGGAGCTGCGAGCCAGGTGGCATCAA 4198  
Db 4082 ACAGCACTGGTCAGAGACTAAGAAATTCAGATTTTGGAGCTGCGAGCCAGGTGGCATCAA 4141  
QY 4199 AAGGAACCTGGTCAGGAGAGTTTCAGGACAAATTAAGGACAAATTCAGGACAAATTCAGGAC 4258  
Db 4142 AAGGAACCTGGTCAGGAGAGTTTCAGGACAAATTAAGGACAAATTCAGGACAAATTCAGGAC 4201  
QY 4359 CTGAGGTACTAAGAGGTCAACAGATATGCAAGGACCTGTGATGATGAGTGTGGCTGTG 4318  
Db 4202 CTGAGGTACTAAGAGGTCAACAGATATGCAAGGACCTGTGATGATGAGTGTGGCTGTG 4261  
QY 4319 CTATATAGAAATGGCTTGTCAAACACCATGCAATGCAATGCAATGCAATGCAATGCAATG 4378  
Db 4262 CTATATAGAAATGGCTTGTCAAACACCATGCAATGCAATGCAATGCAATGCAATGCAATG 4321  
QY 4379 TTGCTTTGATATTTAAGATTCCTAGTGCACACTGCTCCATCGATCCCTTCACATTTGT 4438  
Db 4322 TTGCTTTGATATTTAAGATTCCTAGTGCACACTGCTCCATCGATCCCTTCACATTTGT 4381  
QY 4439 CTCCTGGTTACGAGATGGCTCTTCGTTGTTTGTAGAACTTCAACCTCAGACAGACCTC 4498  
Db 4382 CTCCTGGTTTACGAGATGGCTCTTCGTTGTTTGTAGAACTTCAACCTCAGACAGACCTC 4441  
QY 4499 CATCAAGAGACTACTGAAGCATCCAGTCTTTCGTACTACATGTTAG 4545  
Db 4442 CATCAAGAGACTACTGAAGCATCCAGTCTTTCGTACTACATGTTAG 4488

## RESULT 6

AA566059  
ID AA566059 standard; cDNA; 4492 BP.  
AC AA566059;  
DT 13-FEB-2002 (first entry)  
DE DNA encoding novel human diagnostic protein #1863.  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US008631.  
XX 31-MAR-2000; 2000US-00540217.  
XX 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
XX P-P8DB; ABG01872.

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

PS Claim 1; SEQ ID NO 1863; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement (II) and its binding partners are useful in medical disorders  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activities. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AA564197-AA594564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 4492 BP; 1266 A; 1057 C; 1101 G; 1067 T; 0 U; 1 Other;

Query Match 83.0%; Score 4354; DB 5; Length 4492;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 4445; Conservative 0; Mismatches 36; Indels 10; Gaps 6;  
QY 65 CGAGCCCTGAGGACGCGCGCGGAGGAGCCCTCAAGCGAGAGCGCGCGCGGCTG 124  
Db 2 CGAGCCCTGAGGACGCGCGCGGAGGAGCCCTCAAGCGAGAGCGCGCGCGGCTG 61  
QY 125 CGCGGGACTGCTGGGAGGCGGCGCGGAGGCGGCGGAGCGGCGGAGCTGGCGCGC 184  
Db 62 CGCGGGACTGCTGGGAGGCGGCGCGGAGGCGGCGGAGCGGCGGAGCTGGCGCGC 121  
QY 185 GGCAGCTGCGCAAGTGGCGAGTGGAGCTGGAGCTGGAGCTGGAGCGCGCTTCC 244  
Db 122 GGCAGCTGCGCAAGTGGCGAGTGGAGCTGGAGCTGGAGCGCGCTTCC 181  
QY 245 TTGCGCCCTCAGCGCGCGCTCTCGACTTCCCGCGCGGAGCGCGGAGCGCGCGG 304  
Db 182 TTGCGCCCTCAGCGCGCGCTCTCGACTTCCCGCGCGGAGCGCGGAGCGCGCGG 241  
QY 305 GAGTGGGACCGGCTTCCAGCGCTGGCGGCTGGCGCGCGCGCGCGAGCGCGCGG 364  
Db 242 GAGTGGGACCGGCTTCCAGCGCTGGCGGCTGGCGCGCGCGCGCGAGCGCGCGG 301  
QY 365 GCGCGCCCACTTACCGAGTGGCGCGCGCGGAGCGCGGCGCGCTCGAGTCCCGCG 424  
Db 302 GCGCGCCCACTTACCGAGTGGCGCGCGCGGAGCGCGGCGCGCTCGAGTCCCGCG 361  
QY 425 CGGCGGAGCGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCTCTCTCGAGCGCGCGCG 484  
Db 362 CGGCGGAGCGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCTCTCTCGAGCGCGCGCG 421  
QY 485 CGGCTGCTGAGATGGAGATAAAGAACTCTCAAGGGGTTCACAGATGATGATCGTC 544  
Db 422 CGGCTGCTGAGATGGAGATAAAGAACTCTCAAGGGGTTCACAGATGATGATCGTC 481  
QY 545 CAGAGGAACGAATGATCAGGAGAACTGAAGGCAACCTGTATGCCAGCTGGAAGCAGC 604  
Db 482 CAGAGGAACGAATGATCAGGAGAACTGAAGGCAACCTGTATGCCAGCTGGAAGCAGC 541  
QY 605 AATGGTTGGAAGAGGAGAAATAGCGGAGCGCTGTGTGTGTAAACCAATCCCGTTAAG 664  
Db 542 AATGGTTGGAAGAGGAGAAATAGCGGAGCGCTGTGTGTGTAAACCAATCCCGTTAAG 601  
QY 665 GAGATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCCAGGAGAGGTCAGCAGG 724  
Db 602 GAGATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCCAGGAGAGGTCAGCAGG 661  
QY 725 CGGCTTCCAGGCTTCCAAAGCGCGAGCTGCTTCTCTGGCAACTCCCGATCAGGTC 784



Db 662 CGGCTTCCACGCTTCCAAAGCCGAGCGAGTCCTCTCTCGTCCAACTCCCCATCAGGTC 721  
Qy 785 GCACAGTGAATCAGATCTCCAGAGGTAGGAGAGAAAGATTTCCCCAGTGCCTTTTC 844  
Db 722 GCACAGTGAATCAGATCTCCAGAGGTAGGAGAGAAAGATTTCCCCAGTGCCTTTTC 781  
Qy 845 AGAGTGGCAGAAATCACACCCACCCGAGAGAGCCCTTCCACAGATGGCTTTCCACCATATA 904  
Db 782 AGAGTGGCAGAAATCACACCCACCCGAGAGAGCCCTTCCACAGATGGCTTTCCACCATATA 841  
Qy 905 GCCCTGAGAAACAAACCCGCTGTAAACAAAGTATGCGGGCCAGACTGTACTTACTGC 964  
Db 842 GCCCTGAGAAACAAACCCGCTGTAAACAAAGTATGCGGGCCAGACTGTACTTACTGC 901  
Qy 965 AGCAGATAGGCTAACTCTCTTCTGATTTGAGGAGAGAGCCCAAGACAAATAAATACCGGG 1024  
Db 902 AGCAGATAGGCTAACTCTCTTCTGATTTGAGGAGAGAGCCCAAGACAAATAAATACCGGG 961  
Qy 1025 TGTATATTTGGCCCTCAGAACTGCAGCTGTGACGTGGAACTCTGTATTATCATCTGTAT 1084  
Db 962 TGTATATTTGGCCCTCAGAACTGCAGCTGTGACATGTGAACTCTGTATTATCATCTGTAT 1021  
Qy 1085 TTGTGATGCTCGGGTGTTCCTCAACTAGAACCTTCAGACCCCAATGTTATGGAGAAAACTT 1144  
Db 1022 TTGTGATGCTCGGGTGTTCCTCAACTAGAACCTTCAGACCCCAATGTTATGGAGAAAACTT 1081  
Qy 1145 TAAAGAAATTTGAGGTTGAGAGTTTGTTCAGAAATATCAGTAGGGGTAGCTCAAGGA 1204  
Db 1082 TAAAGAAATTTGAGGTTGAGAGTTTGTTCAGAAATATCAGTAGGGGTAGCTCAAGGA 1141  
Qy 1205 TCAAGAGCTCCATCTCGTAAACACCATCCAGAAAGTTTGTTCACGCAATGTCAAATCTCAT 1264  
Db 1142 TCAAGAGCTCCATCTCGTAAACACCATCCAGAAAGTTTGTTCACGCAATGTCAAATCTCAT 1201  
Qy 1265 CATTTGATCATCTAGTACTTCTAGTCTAGTTTCAAGAAACAGCATAAAGGATCAAGAG 1324  
Db 1202 CATTTGATCATCTAGTACTTCTAGTCTAGTTTCAAGAAACAGCATAAAGGATCAAGAG 1261  
Qy 1325 AACAGATGTCTCTATTTGCTGTGGGCTGTTGATGAAGAAAGTCTTACAGTGTGTG 1384  
Db 1262 AACAGATGTCTCTATTTGCTGTGGGCTGTTGATGAAGAAAGTCTTACAGTGTGTG 1321  
Qy 1385 AAGAGGCTGAGGAAACAGCTGACACCACTGATGTCTAAATTTGGGCAAGAGTGA 1444  
Db 1322 AAGAGGCTGAGGAAACAGCTGACACCACTGATGTCTAAATTTGGGCAAGAGTGA 1381  
Qy 1445 GAAGAAATAGAAACCTTTAATGTCCCTTTGTAGATCTAAGTGGAGATCTCATGAT 1504  
Db 1382 GAAGAAATAGAAACCTTTAATGTCCCTTTGTAGATCTAAGTGGAGATCTCATGAT 1441  
Qy 1505 TCTACAGCCAAGTGTCAAGTCTGTGTGATTTCCCTTCTTCCCTCAGAGTGCACAGC 1564  
Db 1442 TCTACAGCCAAGTGTCAAGTCTGTGTGATTTCCCTTCTTCCCTCAGAGTGCACAGC 1501  
Qy 1565 AGCAAAACCTTACAGCAGAGCCCTTTGGCTGGATCAGAGGAATCAAGAGAGCAATTTTA 1624  
Db 1502 AGCAAAACCTTACAGCAGAGCCCTTTGGCTGGATCAGAGGAATCAAGAGAGCAATTTTA 1561  
Qy 1625 ACCTTACTCATTATGGAATCAGAAATCCCTCTGCTTACAAAGATTTAGCTAGCCAT 1684  
Db 1562 ACCTTACTCATTATGGAATCAGAAATCCCTCTGCTTACAAAGATTTAGCTAGCCAT 1621  
Qy 1685 GGNATTCAGGTGTGGAATGGAATCGTTGGCTGCTTATTTCTAGAACTGGATGTGA 1744  
Db 1622 GGNATTCAGGTGTGGAATGGAATCGTTGGCTGCTTATTTCTAGAACTGGATGTGA 1681  
Qy 1745 GAGAGATGGCCCTCAGGCGTCTTTTCCCATGATGTACAGTGGGGCCCTGCTGTGGCAATG 1804  
Db 1682 GAGAGATGGCCCTCAGGCGTCTTTTCCCATGATGTACAGTGGGGCCCTGCTGTGGCAATG 1741  
Qy 1805 GGGAGAGCACTGAATTTCTGGGGCAGCAGTGGAGCAGCCGAGTGGGGAGCCACCA 1864  
Db 1742 GGGAGAGCACTGAATTTCTGGGGCAGCAGTGGAGCAGCCGAGTGGGGAGCCACCA 1801

Qy 1865 GTGGGTCTTCCAGACCAGTATCTCAGGAGATGTGGTGGAGGCATGTCTGAGCGTTCGT 1924  
Db 1802 GTGGGTCTTCCAGACCAGTATCTCAGGAGATGTGGTGGAGGCATGTCTGAGCGTTCGT 1861  
Qy 1925 CAATGGTCTGTCTGACCCCTGTCTACAAAGTGTAGTGTCTTAAACATTTGAGAG 1984  
Db 1862 CAATGGTCTGTCTGACCCCTGTCTACAAAGTGTAGTGTCTTAAACATTTGAGAG 1921  
Qy 1985 CCATGTGTATATATCTCTTCCACAGTGTTCAGCGAAAGAAATCAAACTTCAGAGACTTC 2044  
Db 1922 CCATGTGTATATATCTCTTCCACAGTGTTCAGCGAAAGAAATCAAACTTCAGAGACTTC 1981  
Qy 2045 TCCAGCCAGTTGTAGACACCACTCTAGTCAAAATGTGCAAGATGCCAATAGCCGCAAGTC 2104  
Db 1982 TCCAGCCAGTTGTAGACACCACTCTAGTCAAAATGTGCAAGATGCCAATAGCCGCAAGTC 2041  
Qy 2105 AGCTGTCCATATCAACACTGTTTGGAACTGTGCAAAAGGCCAAAGCAGAGAGTTGGCAGTTG 2164  
Db 2042 AGCTGTCCATATCAACACTGTTTGGAACTGTGCAAAAGGCCAAAGCAGAGAGTTGGCAGTTG 2101  
Qy 2165 GCAGAGAAATATCAAAAGCTGGATCCATTTGGTGTATTTGGTGTGATTTATGCTTTAAAT 2224  
Db 2102 GCAGAGAAATATCAAAAGCTGGATCCATTTGGTGTATTTGGTGTGATTTATGCTTTAAAT 2161  
Qy 2225 GTATTTCTTGGAAACCAAACTGAATCAAACTGAATTTGGCAAGAACTTCTTGGCCGCTTTGTC 2284  
Db 2162 GTATTTCTTGGAAACCAAACTGAATCAAACTGAATTTGGCAAGAACTTCTTGGCCGCTTTGTC 2221  
Qy 2285 TTATAGATAGACTGTTTGGAAATTTCTGCTGAAATTTATCTCTATTTGTCAGTACTG 2344  
Db 2222 TTATAGATAGACTGTTTGGAAATTTCTGCTGAAATTTATCTCTATTTGTCAGTACTG 2281  
Qy 2345 ATGTTTCAAGCTGAGCCTGTTGAAATCAGGTATATAAGAGCTGTCTTCTTTAACT 2404  
Db 2282 ATGTTTCAAGCTGAGCCTGTTGAAATCAGGTATATAAGAGCTGTCTTCTTTAACT 2341  
Qy 2405 TTGCTTTGCACTGTTGTAATTTCCACTCAATGGTGGCAAACTTTCCAGAGAGTCT 2464  
Db 2342 TTGCTTTGCACTGTTGTAATTTCCACTCAATGGTGGCAAACTTTCCAGAGAGTCT 2401  
Qy 2465 ACTTTGAGTTCTGCAAGATGTTTACTACAGTACCCCATGTTTTCAAAACCTTTAGAAA 2524  
Db 2402 ACTTTGAGTTCTGCAAGATGTTTACTACAGTACCCCATGTTTTCAAAACCTTTAGAAA 2461  
Qy 2525 TGTGAGTGTTCAG ---TTCCACTCACTTCCAGAGTGTCTGCGCTTTGATGGCTA 2581  
Db 2462 TGTGAGTGTTCAGTGTTCCTCACTTCCAGAGTGTCTGCGCTTTGATGGCTT 2521  
Qy 2582 TTGAGATGAGTGGGAAATTTCCGAGCCATCCAGTTGGGCGTAGAAGACACTTTTGGATG 2641  
Db 2522 ATGAGATGAGTGGGAAATTTCCGAGCCATCCAGTTGGGCGTAGAAGACACTTTTACAC 2581  
Qy 2642 GTCAACAGGACAGC ---TTCTTGGAGGCATCTGTTCCCAACACTATCTGGAACCCACAG 2699  
Db 2582 GACAAACAACAACAGCTTTTGCAGGCATCTGTTCCCAACAACACTATCTGGAACCCACAG 2641  
Qy 2700 GAACAGTTCCTCC ---TGAGTGCACAGTCCATTTAGAGAAACTGGAAAAGGATTTATGCTA 2758  
Db 2642 GAACAGTTCCTCCCTTGAGTGCAAGTCCATTTAGAGAAACTGGAAAAGGATTTATGCTA 2701  
Qy 2759 CAAAAATTTGAGTGGCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGCATTTTCACTAGTAGGAC 2818  
Db 2702 CAAAAATTTGAGTGGCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGGATTTTCACTAGTAGGAC 2761  
Qy 2819 CTCTAGTTTCAACAAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 2878  
Db 2762 CTCTAGTTTCAACAAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 2821  
Qy 2879 CAAAAGGAGAGAGCCCAAGTGTGAGTGTGAACTCTCTCTTTATCTCATTCATTCCTCAAT 2938  
Db 2822 CAAAAGGAGAGAGCCCAAGTGTGAGTGTGAACTCTCTCTTTATCTCATTCATTCCTCAAT 2881

QY 2939 TAATGTTTCCAGCCTTGTCAACCCCTTCTTCTTACCCCATCTGTACAGCTGGCACTG 2998  
Db 2882 TAATGTTTCCAGCCTTGTCAACCCCTTCTTCTTACCCCATCTGTACAGCTGGCACTG 2941  
QY 2999 CAACAGATGCTCTTAAGCATAGACTTCAGGGATTCATTCCTGAGAAATACCTTCTGCAT 3058  
Db 2942 CAACAGATGCTCTTAAGCATAGACTTCAGGGATTCATTCCTGAGAAATACCTTCTGCAT 3001  
QY 3059 CTCCTCAAAACACAGCGCAAGTTTCTCTTACCAATTCACAGAAACTGTCCTGAAAACAAAG 3118  
Db 3002 CTCCTCAAAACACAGCGCAAGTTTCTCTTCAATTCACAGAAACTGTCCTGAAAACAAAG 3061  
QY 3119 ACTCAGATAAATTTCCCCAGTCTTTACTCAGTCAAGACCTTGCCTTCCAGTAAACATAC 3178  
Db 3062 ACTCAGATAAATTTCCCCAGTCTTTACTCAGTCAAGACCTTGCCTTCCAGTAAACATAC 3121  
QY 3179 ACAGGCCAAAGCCATCTAGACCTACCCAGGTATACAAAGTAACACAGGGATCCCTCAA 3238  
Db 3122 ACAGGCCAAAGCCATCTAGACCTACCCAGGTATACAAAGTAACACAGGGATCCCTCAA 3181  
QY 3239 AAAATAGCATGACATTTGATCTGAACAGTAGTTCAAAATGTGATGACAGCTTTGGCTGTA 3298  
Db 3182 AAAATAGCATGACATTTGATCTGAACAGTAGTTCAAAATGTGATGACAGCTTTGGCTGTA 3241  
QY 3299 GCAGCAATAGTAGTAATGCTGTATACCCAGTGCAGACAGTGTTCACCCCACTAGAGG 3358  
Db 3242 GCAGCAATAGTAGTAATGCTGTATACCCAGTGCAGACAGTGTTCACCCCACTAGAGG 3301  
QY 3359 AGAAATGCAGATTAGATGTCAATACAGAGCTCAACTCCAGTATTGAGGACCTTCTTGAAG 3418  
Db 3302 AGAAATGCAGATTAGATGTCAATACAGAGCTCAACTCCAGTATTGAGGACCTTCTTGAAG 3361  
QY 3419 CATCTATGCTTCAAGTATACAAACAGTAACTTTTAAAGTCAAGAGTTGCTGCTGCTC 3478  
Db 3362 CATCTATGCTTCAAGTATACAAACAGTAACTTTTAAAGTCAAGAGTTGCTGCTGCTC 3421  
QY 3479 CTCGAAAGGCTGAAATGATGATACCTCAAGATGATGTGAATCATTAATCAAAAGTGCA 3538  
Db 3422 CTCGAAAGGCTGAAATGATGATACCTCAAGATGATGTGAATCATTAATCAAAAGTGCA 3481  
QY 3539 AAGAGAAGATGAAAGCTGAAGAAAGAGCTTTTAGCAATTTGCCATGGCAATGTGACGGT 3598  
Db 3482 AAGAGAAGATGAAAGCTGAAGAAAGAGAGCTTTTAGCAATTTGCCATGGCAATGTGACGGT 3541  
QY 3599 CTCAGATGCCCTCCCATAGTTCTCAGTGCAGGTTGAAATGGAGAAGATATCATCA 3658  
Db 3542 CTCAGATGCCCTCCCATAGTTCTCAGTGCAGGTTGAAATGGAGAAGATATCATCA 3601  
QY 3659 TTATTCAACAGGAATACACAGAGACTCTACAGGACATACCAAGCAAAACACCGTATA 3718  
Db 3602 TTATTCAACAGGAATACACAGAGACTCTACAGGACATACCAAGCAAAACACCGTATA 3661  
QY 3719 GAGAGACACTCAATGGCTGAAGGTCAACAGATAGGCTTGGAGCATTTTCTTCTTGT 3778  
Db 3662 GAGAGACACTCAATGGCTGAAGGTCAACAGATAGGCTTGGAGCATTTTCTTCTTGT 3721  
QY 3779 ATCAGGCTCAAGATGTGGAACTGGAACCTTTAATGGCTGTTAAACAGGTGACTTATGTCA 3838  
Db 3722 ATCAGGCTCAAGATGTGGAACTGGAACCTTTAATGGCTGTTAATCAAGGTGACTTATGTCA 3781  
QY 3839 GAAACACATCTTCTGAGCAAGAGAGTATAGAGACTTAAGAGAAAGATTAAGTCA 3898  
Db 3782 GAAACACATCTTCTGAGCAAGAGAGTATAGAGACTTAAGAGAAAGATTAAGTCA 3841  
QY 3899 TGAGCCATCTGAATCATCAAAACATCATTAGATGTTGGAGCCACGTTGAGAAGAGCA 3958  
Db 3842 TGAGCCATCTGAATCATCAAAACATCATTAGATGTTGGAGCCACGTTGAGAAGAGCA 3901  
QY 3959 ATTACAACTCTTCTATGAATGGATGGAGGGGATCGGTGGCTCATTTGCTGAGTAAAT 4018  
Db 3902 ATTACAACTCTTCTATGAATGGATGGAGGGGATCGGTGGCTCATTTGCTGAGTAAAT 3961  
QY 4019 ATGGAGCCTTCAAGAAATCAGTAGTTATTAACACTACACTGAACAGTACTCCCGTGGCCTTT 4078

Db 3962 ATGGAGCCTTCAAGAAATCAGTAGTTATTAACACTACACTGAACAGTACTCCGTGGACTTT 4021  
QY 4079 CGTATCTCATGAAAAACCAAAATCATTCACAGAGATGTCAAAGTGCCAAATTTGCTAATG 4138  
Db 4022 CGTATCTCATGAAAAACCAAAATCATTCACAGAGATGTCAAAGTGCCAAATTTGCTAATG 4081  
QY 4139 ACAGCACTGGTCAGAGACTTAAGAAATTTGGAGCTGCAGCCAGGTTGGCATCAA 4198  
Db 4082 ACAGCACTGGTCAGAGACTTAAGAAATTTGGAGCTGCAGCCAGGTTGGCATCAA 4141  
QY 4199 AAGGAACTGGTCAGAGAGATTTTCAGGGAACAATTAATCTGGGACAATTCGATTTATGGCAC 4258  
Db 4142 AAGGAACTGGTCAGAGAGATTTTCAGGGAACAATTAATCTGGGACAATTCGATTTATGGCAC 4201  
QY 4259 CTGAGGTATTAAGAGCTCAACAGTATGGAAGAGAGCTGTGATGTATGGAGTGTGGCTGTG 4318  
Db 4202 CTGAGGTATTAAGAGCTCAACAGTATGGAAGAGAGCTGTGATGTATGGAGTGTGGCTGTG 4261  
QY 4319 CTATTATAGAAATGGCTTGTGCAAAACCAACCACTGGAATGCAGAAAACAACCTCAATCATC 4378  
Db 4262 CTATTATAGAAATGGCTTGTGCAAAACCAACCACTGGAATGCAGAAAACAACCTCAATCATC 4321  
QY 4379 TTGCTTTGATATTTAAGATTTGCTAGTGCAACTTCTCCATCGATCCCTTCACATTTGT 4438  
Db 4322 TTGCTTTGATATTTAAGATTTGCTAGTGCAACTTCTCCATCGATCCCTTCACATTTGT 4381  
QY 4439 CTCCTGGTTACG-AGATGTGCTCTTCTGTTGTT-AGAACTTCAACCT--CAGGACAGA 4494  
Db 4382 CTCCTGGTTTACGAAGATGTGGCTCTTCTGTTGTTTAAAGAACTTCAACCTTCANGGACAGA 4441  
QY 4495 CTTCCATCAAGAGAGCTACTGAAGCATCCAGTCTTTTCGTACTACATGGTAG 4545  
Db 4442 CTTCCATCAAGAGAGCTACTGAAGCATCCAGTCTTTTCGTACTACATGGTAG 4492

## RESULT 7

ABT42340

ID ABT42340 standard; DNA; 5180 BP.

XX AC ABT42340;

XX DT 26-JUN-2003 (first entry)

XX Toxicity modelling related rat gene SEQ ID No 2042.

XX Toxic effect; gene expression profile; renal toxicity; toxicity marker;  
XX database; drug screening; toxicity assay; rat; ds.

XX OS Rattus norvegicus.

XX PN W0200295000-A2.

XX PD 28-NOV-2002.

XX PF 22-MAY-2002; 2002W0-US016173.

XX PR 22-MAY-2001; 2001US-0292335P.

XX PR 13-JUN-2001; 2001US-0297523P.

XX PR 19-JUN-2001; 2001US-0298925P.

XX PR 10-JUL-2001; 2001US-0303807P.

XX PR 10-JUL-2001; 2001US-0303808P.

XX PR 28-AUG-2001; 2001US-0303810P.

XX PR 27-SEP-2001; 2001US-0324928P.

XX PR 22-OCT-2001; 2001US-0330462P.

XX PR 01-NOV-2001; 2001US-0330867P.

XX PR 21-NOV-2001; 2001US-0331805P.

XX PR 06-DEC-2001; 2001US-0336144P.

XX PR 19-DEC-2001; 2001US-0340873P.

XX PR 21-FEB-2002; 2002US-0357842P.

XX PR 21-FEB-2002; 2002US-0357843P.

XX PR 21-FEB-2002; 2002US-0357844P.



QY 1561 CAGCAGCAAAACCGTACAGCAGCAGCCTTTGGCTGGATCA---CGAAGGAATCAAGAGAGC 1617  
Db 2040 CAGCAGCCCTCCTCCCGCAACAGCCTGTGSCCGGATCACAGCGGAGGAATCAGGAAGC 2099  
QY 1618 AATTTTAACCTTACTCATTAATGGAATCAGCAATCCCTGCTGTCTTACAAGATTTAGCT 1677  
Db 2100 AATTTTAACCTTACTCATTAATGGAATCAGCAATCCCTGCTGTCTTACAAGATTTAGCC 2159  
QY 1678 GAGCATGGATTCAAGGTGTTTGGAAATGGAATCCGTGGCTGCTTATTTTCTAGAAACTGG 1737  
Db 2160 GAGCCATGGATTCAAGCAATTCGGAATGGAGCTCGTTGGCTGCTTATTTCTAGAACTGG 2219  
QY 1738 AATGTGAGAGATGGCCCTCAGCGGCTTTTCCCATGATGTCAGTGGGGCCCTGCTGTTG 1797  
Db 2220 AACGTAAAGGAGATGGCCCTTAGCGGCTTTTCCACGATGTTAGCGGGGCCCTGTTGTTG 2279  
QY 1798 GCAATGGGAGAGACACTGGAAATTTCTGGGGGAGCAGTGGAGCAGCCCGAGTGGGGGA 1857  
Db 2280 CGGAACGGGAGAGACACTGGAACTTTCTGGAGCGGAGCGGAGCGCACTAAGTGTGGC 2339  
QY 1858 GCCACCAAGTGGTCTTCCAGACAGTATCTCAGAGATGTGGTGGAGGATGCTGCAGC 1917  
Db 2340 GCCGCCAGTGGTCTTCCAGCCAGCATCTCAGGGGACGTGTGGAGGCGTTCGCGAGC 2399  
QY 1918 GTTCTGTCAATGGTCTGTGCTGACCCCTGTCTACAAAGTGTACGTGCTGCTTTAAABA 1977  
Db 2400 GTCTGTCTATCGTGTGGCTGTGACCCCTGTCTACAAAGTGTACGTGCTGCTTTAAABA 2459  
QY 1978 TTGAGAGCCATGCTGGTATATPACTCTTGGCCACAGTGTAGCGGAAAGAAATCAAACTTCAG 2037  
Db 2460 CTGAGAGCCATGCTGGTATACACTCTTGGCCACAGCCTGGCAGAAAGAAATCAAACTTCAG 2519  
QY 2038 AGACTTCCAGCCAGTGTGTAGACACCATCTAGTCAATGTGCAGATGCCATAGCCGC 2097  
Db 2520 AGACTTCCAGCCAGTGTGTAGACACCATCTAGTCAATGTGCAGATGCCATAGCCGC 2579  
QY 2098 ACAAGTCAAGTGTCCATATCAACTGTGTGAACTGTGCAAGGCCAAGCAGAGAGATTG 2157  
Db 2580 ACGAGTCAAGTGTCCATATCAACTGTGTGAGCTGTGCAAGGCCAAGCGGGGAGTTG 2639  
QY 2158 GCAGTTGCAGAGAAATCTAAAGCTGGATCCATGTGATTTGTTGTTGATTTATGTC 2217  
Db 2640 GCAGTTGCAGAGAAATCTAAAGCTGGATCCATGTGTTGTTGTTGATTTATGTC 2699  
QY 2218 TTAAATCTGATTTCTTGGAAACCAAACTGAATCAAACTTGGCAAGAACTTCTTGGCCGC 2277  
Db 2700 TTAAATCTGATTTCTTGGAAACCAAACTGAATCAAACTTGGCAAGAACTTCTTGGCTGC 2759  
QY 2278 CTTTGTCTTATAGATAGACTGTGTGGAATTTCTGCTGAATTTTATPCTCATATTGTC 2337  
Db 2760 CTTTGTCTTATAGACAGATTGCTCTTGGAAATTTCTGCGGAATTTTATCCTCATATTGTC 2819  
QY 2338 AGTACTGATGTTTACAGCTGAGCCTGTGGAATCAGGTATAGAGCTGCTGCCCTC 2397  
Db 2820 AGTACCGATGTTCTCAAGCCGAGCCTGTGGAATCAGGTATAGAGCTGCTGCCCTC 2879  
QY 2398 TTAACTTTGCTTTGCACTCCATTTGATAATTTCCCACTCAATGGTGGCAAACTTTCCAGA 2457  
Db 2880 TTAGCCTTTGCTTTGCAATCCATTTGACAATTTCCCACTCTATGGTGGCAAACTCTGCGG 2939  
QY 2458 AGGATCTACTGAGTGTGCAAGATGTTTACTACAGTACCCCATGTTTTCAAAAC 2517  
Db 2940 AGGATTTACTGAGCTCAGCAGAAATGGTGTACCAAGTGGCCCTGTTTTCAGCTG 2999  
QY 2518 TTAGAAATGCTGAGTGTGTTCCAGTTCCACTCACCTTCCAGGATGCGTGGCGTTTGATG 2577  
Db 3000 GTAAACCATGCTAAGTGTCTTGGATCTTCCCATCTTCGCCAGGATGGCCGCGTCTGATG 3059  
QY 2578 GCTATTGAGATGAGGTGGAATTTCCGAAAGCCATTCAGTGTGGGCTAGAAAGACACTTTG 2637  
Db 3060 GCCATTGCAGAGAGTGAATTTCCGAGGTCTATCCAGCTGCGGTTTCGGAAGACACTTTG 3119

QY 2638 GATGCTCAACAGCAGCAGCTTCTTGAGGCATCTGTTCCTCAACAACTATCTGSAACACCA 2697  
Db 3120 GATGCTCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3167  
QY 2698 GAGAAAGCTTCCCTGAGTGGACAGTCCATTTAGAAAGAACTGGAAAGAGTATGTCT 2757  
Db 3168 GAGAGCAGCTCCCTTGGACACACGCCATGTAGAAAGAACTGGAAAGAGTATTAAGCT 3227  
QY 2758 ACAAAATTTGAGTGGCCAGTTCAGAGGACATTTCTGAGAGACTGGCCAGCATTTTCA 2817  
Db 3228 ACGAGACTGAGTGGCCAGCTCAGAGGACATTTCTGACAGACTGGCTGGGCTTCTGTAG 3287  
QY 2818 CTTCTTGTGTTTCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA 2877  
Db 3288 CTTCTCTAGTTCA-----GCAACAAACAAACAAACAAACAAACAAACAAACAAAC 3332  
QY 2878 ACAAAAGGAGAGCCCAACAGCTCAGTGTGTTGAACCTCTCTCTTTATCTCATCATTTCC 2937  
Db 3333 ACAAAAGGAGAGCCCAACAGCTCAGTGTGTTGAACCTCTCTCTTTGTTGTTCTCTCTC 3389  
QY 2938 TTAATGTTTCCAGCCTTGTCAACCCCTTCTTCTTCTACCCATCTGTACAGCTGGCCT 2997  
Db 3390 TTAATGTTTCCAGCAATATCAGCCCACTGTTTCACTGCCCCGTCTGTCTCCAGCTGG 3449  
QY 2998 GCAACAGATGCTCTAAGCATAGACTTCAGGATTCATTCCCTGCAGAACTACTCTCTGA 3057  
Db 3450 GTAAACAGATGCTCTAAGCATAGACTTCAGGATTCATTCCCTGCAGAACTACTCTCTGA 3509  
QY 3058 TCTCTCTAAACACAGCGGAAGTTTCTCTAACAATTCACAGAACTGTCTGAAACAA 3117  
Db 3510 TCTCTCTAAACACAGCGGAAGTTTCTCTAACAATTCACAGAACTGTCTGAAACAA 3569  
QY 3118 GACTCAGATAAACTTTCCCTCAGTCTTACTCAGTCAAGACCTTCCCTCAGTAAACATA 3177  
Db 3570 GACTCAGATAAACTTTCCCTCAGTCTTACTCAGTCAAGACCTTCCCTCAGTAAACATA 3629  
QY 3178 CACAGCCAAAGCCATCTAGACTTACCCAGGTAAATACAAGTAACACAGGAGATCCCTCA 3237  
Db 3630 CACAGCCAAAGCCATCTAGACTTACCCAGGTAAATACAAGTAACACAGGAGATCCCTCA 3689  
QY 3238 AAAATAGATCAGACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3297  
Db 3690 AAAATAGATCAGACTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 3749  
QY 3298 AGCAGCAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3357  
Db 3750 GGCAGCAACAGTGGCAGCGCGCTCATACCCAGTGGAGGAGCGCATTCACCCAGCAGAG 3809  
QY 3358 GAGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3417  
Db 3810 GACAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3869  
QY 3418 GCATCTATGCTTCAAGTGAATCAACAGTAACCTTTTAAAGTCAAGATGCTGCTGCTCT 3477  
Db 3870 GCATCTATGCTTCAAGTGAATCAACAGTAACCTTTTAAAGTCAAGATGCTGCTGCTCT 3929  
QY 3478 CTTGAAAGGCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3537  
Db 3930 CTTGAAAGGCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3989  
QY 3538 AAGAGCAAGTGGAGCTGAAGAAGAGCTTTTAGCAATTTGCAATTTGCAATTTGCAAGC 3597  
Db 3990 AAGAGCAAGTGGAGCTGAAGAAGAGCTTTTAGCAATTTGCAATTTGCAATTTGCAAGC 4049  
QY 3598 TCTCAGGATGCCCTCCCCATAGTTCTCAGCTGCGAGGTTGAAAAATGGAGAGATATCAT 3657  
Db 4050 TCTCAGGATGCCCTCCCCATAGTTCTCAGCTGCGAGGTTGAAAAATGGAGAGATATCAT 4109  
QY 3658 ATTATTTCAAGAGTATACACAGAGCTCTACAGGACATACCAAGCAAAACAAACCGTAT 3717  
Db 4110 ATCATCCAGAGATACACAGAGCTCTACAGGACATACCAAGCAAAACAAACCGTAT 4169  
QY 3718 AGAGAAAGACTCAATGGCTGAAAGGTCAACAGATAGGCTTTGGAGCATTTTCTTCTTGT 3777

Db 4170 AGAAGACACCGAGTGGCTGAAAGGGGACAGATAGCCCTCGGAGCATTTCTTCTGT 4229  
Qy 3778 TATCAGGCTCAAGATGTGGGAACATGGAATTTAATGCTGTGTTAAACAGGTGCACTTATGTC 3837  
Db 4230 TACCAAGCACAGGATGTGGGACATGGAATTTAATGCTGTGAAACAGGTGACCTAGTC 4289  
Qy 3838 AGAAGACATCTTCTGAGCAGAGAGAGTAGTAGAGCACTAAGAGAGAGATAGAGATG 3897  
Db 4290 AGAAGACATCTTCTGAGCAGAGAGAGTAGTAGAGCACTTGAAGCCCTTGAAGGAGAGATCAGGATG 4349  
Qy 3898 ATGAGCCATCTGAATCATCCAAACATCATTAAGGATGTTGGAGCCACGCTGTGAGAGAGC 3957  
Db 4350 ATGAGCCATCTCAACCATCCGAAATCATCATAGGATGTTGGGGCCACGTCGAGAGAGC 4409  
Qy 3958 AATTACAATCTCTTCAATTAATGAATGAGTGCAGGGGATCGGTGGCTCATTTGCTGAGTAAA 4017  
Db 4410 AACTACAACCTCTTCAATGAGTGGGAGCCCTCCGTGGCTCACTCTTTGAGTAAA 4469  
Qy 4018 TATGAGCCTTCAAGAAATCAGTATTAATTAACCTACATGAACAGTTTACTCCGTGGCCTT 4077  
Db 4470 TATGAGCTTTCAAGGAGTCACTGCTCATTAACCTACAGAGCACTTACTCCGTGGCCTT 4529  
Qy 4078 TCGTATCTCCATGAAACCAATCATTTACAGAGATGTTAAAGGTGCCAATTTGCTTAAT 4137  
Db 4530 TCCTATCTCCAGAGAACCATCATTTACAGAGACGTTCAAGGGGCCAATCTGCTCAT 4589  
Qy 4138 GACAGCACTGTCAGAGACTAAGATTCAGATTTGAGCTGCAGACGAGTGGCATCA 4197  
Db 4590 GACAGCACCGTGCAGGCTGAGAAATTCAGACTTCGGTGTGCGGACGAGTTGGCATCC 4649  
Qy 4198 AAAGAACTGTGAGGAGAGTTTCAGGACAATTTACTGGGACAATTTGCAATTTATGCGCA 4257  
Db 4650 AAAGAACTGTGAGGAGAGTTTCAGGACAATTTACTGGGACAATTTGCAATTTATGCGG 4709  
Qy 4258 CCTGAGTACTAAGAGTCAACATGATGGAAGGAGCTGTGATGTAGAGTTGGCTGT 4317  
Db 4710 CCTGAGTACTAAGAGTCAACATGATGGAAGGAGCTGTGATGTAGAGTTGGCTGT 4769  
Qy 4318 GCTATTATAGAAATGGCTGTGCAAAACACCATCGAATGAGAGAAACACATCCAAATCAT 4377  
Db 4770 GCAATTAAGAAATGGCTGTGCAAAACACCATCGAATGAGAGAAACACATCCAAATCAT 4829  
Qy 4378 CTGCTTTGATATTAAAGTGTAGTCACTACTGCTCCATGATGCTCCCTTCACTTTG 4437  
Db 4830 CTGCTTTGATATTAAAGTGTAGTCACTACTGCTCCATGATGCTCCCTTCACTTTG 4889  
Qy 4438 TCTCTGCTTTACGAGATGTGCTCTTCTGTTTGTAGAACTTCAACCTCAGGACAGACCT 4497  
Db 4890 TCCCGGGCTCGGAGAGCTGGCTCTGCTGTTTAGAACTTCAACCTCAGGACAGACCT 4949  
Qy 4498 CCATCAGAGAGCTACTGAAGATCCAGTCTTTGATCTAATGATGATGATGATGATGATG 4557  
Db 4950 CCGTCAAGAGAGCTACTGAAGATCCAGTCTTTGATCTAATGATGATGATGATGATG 5003  
Qy 4558 ATCAACTCAGTAGAAGACAGAGTGTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4617  
Db 5004 -----GCTCAGGTTGCGACACAG-GAAGAGAAATCTCGGCGGACGACCT 5048  
Qy 4618 TGATATTCTACGGCCATGATGCCACTGAAACAGTATGAAACAGGCGGAGTGGGAAACCT 4677  
Db 5049 TGATAGTCTGTGGCC-TCATACCACTGACCAG-----AAGAGGGGCCAGTGGGAGGCCG 5103  
Qy 4678 TACCTAAGTATGATTTGCAAAATCATGATCTGTACCTTAAGTCAAGTATGCAAAAGCCCA 4737  
Db 5104 CACCTAAGCATGTGACTGACAAATCATGA-CTGCACCTGAGCTCGCTGTCAGAGCGGCTA 5162  
Qy 4738 -AACTAGTGCAGAAACTG 4754  
Db 5163 CAACCTGTCAGGAGCTG 5180

RESULT 8

ADB58821  
ID ADB58821 standard; DNA; 5180 BP.  
XX  
AC ADB58821;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Toxicity-related gene, SEQ ID 3847.  
XX  
KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;  
KW drug screening; toxicity assay; ds.  
OS Unidentified.  
XX  
PN WO2003064624-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 31-JAN-2003; 2003WO-US003194.  
XX  
PR 31-JAN-2002; 2002US-00060087.  
PR 15-MAR-2002; 2002US-0364045P.  
PR 15-MAR-2002; 2002US-0364055P.  
PR 30-DEC-2002; 2002US-0436643P.  
XX  
PA (GENE-) GENE LOGIC INC.  
XX  
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;  
XX WPI; 2003-689530/65.  
XX  
PT Predicting a toxic effect of a compound, useful in identifying toxicity  
PT markers in liver tissues or cells for drug screening and toxicity assays,  
PT comprises preparing gene expression profile of tissue or cells exposed to  
PT the compound.  
XX  
PS Claim 1; SEQ ID NO 3847; 1156pp; English.  
XX  
CC The present invention relates to a method for predicting a toxic effect  
CC of a compound. The method comprises preparing a gene expression profile  
CC of a tissue or cell sample exposed to the compound, and comparing the  
CC gene expression profile to a database comprising SEQ ID 1-4925, where  
CC differential expression of the gene indicates at least one toxic effect.  
CC The method is useful for predicting at least one toxic effect of a  
CC compound, predicting hepatotoxicity or the progression of a toxic effect  
CC of a compound, identifying an agent that modulates the onset or  
CC progression of a toxic response, predicting the cellular pathways that a  
CC compound modulates in a cell, and identifying an agent that modulates at  
CC least one activity of a protein. The method and compositions of the  
CC present invention using a database of genes having liver toxin-induced  
CC differential expression are useful in identifying toxicity markers in  
CC liver tissues or cells for drug screening and toxicity assays. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
SQ Sequence 5180 BP; 1225 A; 1521 C; 1443 G; 991 T; 0 U; 0 Other;

Query Match 65.2%; Score 3420.8; DB 9; Length 5180;  
Best Local Similarity 84.5%; Pred. No. 0;  
Matches 4020; Conservative 0; Mismatches 647; Indels 91; Gaps 12;  
Qy 1 GAGAAATGGCGCGCGCGCGGGAATCGCGCTCGTCTCGTCTCGGATTCCTCGGCGCGCAGG 60  
Db 510 GAGAAATGGCGCGCGCGCGCGGATCGCGCTCGTCTCGTCTCGGATTCCTCGGCGCGCAGG 569  
Qy 61 GCTACAGCCCTGAGCAGCGCGCGCGGAGAGCCCTCAAGCCAGCAGCGCGCGCGCG 120  
Db 570 GCGGCGAGCCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 629  
Qy 121 GCTGCGCGCGGACTGCTGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
Db 630 GCGGCGCGGCGCTGCTGCGGAGACTGCGCAGCGCGCGCGCGCGCGCGCGCGCG 689

|    |      |                                                                   |      |
|----|------|-------------------------------------------------------------------|------|
| QY | 181  | CGCGGCGAGCTGCGCAAAAGTCCGAGATGTGAGAGCTGGAACAGAGTGCCTGAGACAGCGCGCTC | 240  |
| DB | 690  | CGGAGAGCTGCGCAAAAGTAAAGAGTGTGGAGCTGGACAGAGTGCCTGGGAGACAGCGCGCTC   | 749  |
| QY | 241  | TTCCCTTCCCGCCTCACCGCCGGCCTCCTCGACTTCCCGGTCCCGAGAGCCCGGGAGCGCA     | 300  |
| DB | 750  | TTCTCTACCCGCCTCGCCGCTGCTCCCATCTACTTCCCGTCCGCGAGCCCGGAGCGC         | 809  |
| QY | 301  | CGGGGAGTGGGACCGGCTTCCAGCTGTGGCGGTGCGCGGCCACAGAGACCGCGAGC          | 360  |
| DB | 810  | GCTGACAGAGAGTGGCTTCCAGCTGCGCGCGGACCGGCACCCCGGAGAGCAGCGAGT         | 869  |
| QY | 361  | CGCGCGCGCCCAACCTTACCGAGTCCGCTGGCGCGCGGACAGCGCGCGCTCGAGTCCC        | 420  |
| DB | 870  | CGTTCGCGCTCCCACTCTGCGAGCTGGCGCGCGCGGACAGCGCGCGCCCGGAGCCCC         | 929  |
| QY | 421  | GCAGCGCGGAGCCCGGGGAGAGCGGGCGCCGCGCGGAGCGGTCTCTGAGAGCGGCC          | 480  |
| DB | 930  | CGGGG-----GCCGAGCGCGCCTCTGAGAGCGGCC                               | 959  |
| QY | 481  | CCCGCCGGTCCGTGAGATGGAGAAATAAGAAATCTCAAAGGGTTGCAACAAGATGGATGAT     | 540  |
| DB | 960  | CCCTCCCGTCCGAGAGATGGAGAAATAAGAAACCCCTCAAGATTGCAACAAGATGGATGAC     | 1019 |
| QY | 541  | CGTCCAGAGGAAACGAATGATCAGGGAGAAATGAGGCAACCTGTATGTCAGAGCTGGAAG      | 600  |
| DB | 1020 | CGCCAGAGAGCGAAATGATCAGGGAGAGCTCAAGCGACCTGTATGCTCGCTCGGAG          | 1079 |
| QY | 601  | CAGGAATGGTTGGAAGAGAGAAATAGCGAGGGCCTGTGTGGTAAACCAATCCCAAGTT        | 660  |
| DB | 1080 | CACAGTGGTTAGAAAGAGAGAAACAGAGAGGGCCCTGTGTGGTGAACAATCCCTATT         | 1139 |
| QY | 661  | AAGGAGATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCCAGAGAGGTCCAGGCA        | 720  |
| DB | 1140 | AAAGAGATGGATCTGAAATGAGTAACTTGGCAGCTGAGTCTCAAGAGAGGGCCAGGCA        | 1199 |
| QY | 721  | AGTCCGCTTCAACAGCTTCCAAAGGCCGACGAGTCTCTTCTCTGGCAACTCCCAATCA        | 780  |
| DB | 1200 | GGCTCTGCTGACACAGCTCCCAAGGGCGGACGAAGCCCGTCTCTGGAAGTCCCAATCA        | 1259 |
| QY | 781  | GGTCGCACAGTGAATCAGAAATCAGAGATCCAGGAGTAAGGAGAAAGAGTTTCCCGAGTGCCT   | 840  |
| DB | 1260 | GGGCGCTCAGGAAGCCGGAATCCCAAGAGTGAACGGAACGAGTGTCCCAAGTGCCT          | 1319 |
| QY | 841  | TTTCAGAGTGGCAGAAATCACACCAACCCGAGAGCCCTTCAACAGATGCTTCTCAACCA       | 900  |
| DB | 1320 | TTTCAGAGTGGCAGAAATCACACCACTCCAGAGACCCCGTCCGAGATGCTTCTCAACG        | 1379 |
| QY | 901  | TATAGCCTCTAGGAAACAAACCGCGGTGTTAAACAAGTGAATGGCGGCGAGCTGTACTTA      | 960  |
| DB | 1380 | TACAGCCGAGAGGAGACGAGCGCGGTGTGNAACAAGTGAATGAGGCGAGCTGTACTTC        | 1439 |
| QY | 961  | CTGCAGCAGATPAGGCTTAACCTTTCTGATTTGGAGAGACAGCCCGAGACAATAATAC        | 1020 |
| DB | 1440 | CTGCAGCAGATPAGGACCAACTCTTTCTGATTTGGAGAGACAGTCCAGACAATAATAC        | 1499 |
| QY | 1021 | CGGTGTTTATTTGGGCTCAGAACTGCAGCTGTCACGTGAACATTTCTGATTCATCTG         | 1080 |
| DB | 1500 | CGGTGTTTATTTGGGCAACAGAACTGCAGCTGTGGGCTGGGACATTTCTGATTCACCTC       | 1559 |
| QY | 1081 | CTATTTGATGCTCCGGGTGTTTCAACTAGAACTTTCAGAGCCCAATGTTTATGGAGAAA       | 1140 |
| DB | 1560 | TTGTTTGTCTATGCTCCGGGTGTTCCAGCTAGAACCTCCGACCCCATGCTATGGAGAAA       | 1619 |
| QY | 1141 | ACTTTAAAGAAATTTGAGTTGAGATTTGTTTCCAGAAAATATCACAGTAGGCTGAGTCA       | 1200 |
| DB | 1620 | ACTTTAAAGAAATTTGAGTTGAGATTTGTTTCCAGAAAATATCACAGTAGGCTGAGTCA       | 1679 |
| QY | 1201 | AGGATCAAGCTCCATCTGTAAACCAATCCAGAAAGTTTGTTCACGAGTGTCAAATCT         | 1260 |
| DB | 1680 | AGAAATCAAGCTCCATCTCGGAACCAATCCAGAAAGTTTGTTCACGAGTGTCAAATCT        | 1739 |

|    |      |                                                                  |      |
|----|------|------------------------------------------------------------------|------|
| Qy | 1261 | CATACATTGCTCATCTCTAGTACTTCTPACGCTTAGTTTCAGAAAAACAGCATATAAGGATGAA | 1320 |
| Db | 1740 | CACACATTTGTCATCGTCTAGCACAATCACATCTAGTTTCAGAAAAACAGCATCAAGGATGAA  | 1799 |
| Qy | 1321 | GAGGAAACAGATGTCCTATTTGCTTGTGGGCATGCTTCATGAAGAAAGCTCTTACAGTG      | 1380 |
| Db | 1800 | GAGGAGCAGATGTCGCCATCTGCTTGTGGGCATGCTGATGAGGAGAGCCTGACTGTG        | 1859 |
| Qy | 1381 | TGTGAAGACGGCTGCAGGAACAAGCTGCACCAACCATCTGCATGTCAATTTGGGCAGAGAG    | 1440 |
| Db | 1860 | TGTGAAGACGGCTGCAGGAACAAGCTGCACCAACCATCTGCATGTCAATTTGGGCAGAGAA    | 1919 |
| Qy | 1441 | TGTAGAGAAATAGAGAAACCTTTAAATATGTCCCTTTTGTAGATCTAAGTGGAGATCTCAT    | 1500 |
| Db | 1920 | TGTAGAGAAATAGAGAAACCGTTAAATATGTCCCTTTTGTAGATCTAAGTGGAGATCCCAT    | 1979 |
| Qy | 1501 | GAATTTCTACAGCACGAGTTGTCAAGTCCTGTGTGATTCGCCCTTCTCCCTCAGAGCTGCA    | 1560 |
| Db | 1980 | GAATTTCTACAGCCATGAGTTTATCAAGCCCTGTGTGATTCGCCCTTCTCCCTGCGAGGTGTA  | 2039 |
| Qy | 1561 | CAGCAGCAAAACCGGTACAGCAGCAGCCTTTGGCTGGATCA---CGAAGGAATCAAGAGAGC   | 1617 |
| Db | 2040 | CAGCAGCCCTCC---CCCGCAACAGCCTGTGGCCGATCACAGCGAGGAATCAGGAAGC       | 2099 |
| Qy | 1618 | AAATTTAAACCTTACTCATTTATGAACTCAGCAAAATCCCTCCCTGCTTCAAGATTTAGCT    | 1677 |
| Db | 2100 | AAATTTAAACCTTACTCATTTATGAAACCCAGAGATTCCTCCCGTTTCAAAAGATTTTACCC   | 2159 |
| Qy | 1678 | GAGCCATGGATTGAGTGTTTGAATTGGAACTCGTTGGCTGCTATTATTTCTAGAAACTGG     | 1737 |
| Db | 2160 | GAGCCATGGATTGAGGCATTCGGAATTGGAGCTGTTGGCTGCTATTCTCTAGAAACTGG      | 2219 |
| Qy | 1738 | AAATGTGAGAGAGATGGCCCTCAGCGCTTTTCCCATGATCTCAGTGGGGGCCCTGCTCTTG    | 1797 |
| Db | 2220 | AAATGTGAGGAGATGGCCCTTAGCGCCCTTCCACGATGTTAGCGGGGCCCTGTTGTTG       | 2279 |
| Qy | 1798 | GCAAATCGGAGAGCACTGGAATTTCTGGGGCAGCAGTGGAAACGACGCCGAGTGGGGGA      | 1857 |
| Db | 2280 | GCGAACCGGAGAGCACTGGAATTTCTTGGAGGGCGGACGCGAGGAGCAGCCTTAAGTCTGGC   | 2339 |
| Qy | 1858 | GCACACAGTGGGTCTTCCACAGACAGATCTCAGGAGATGCTGTTGGAGGCGATGCTGCAGC    | 1917 |
| Db | 2340 | GCAGCAGTGGGTCTTCCAGCCACGATCTCAGGGGACGTTGTTGGAGGCGTTCTGCAGC       | 2399 |
| Qy | 1918 | GTTCTGTCAATGTCGTGTGACCCCTGTTCAAAAGTGTACGTTGCTGTCTTTAAAAACA       | 1977 |
| Db | 2400 | GTCCTGTCTATCGTGTGCGTGACCCCTGTCTACAAAGTGTACGTTGCTGTCTTTAAAAACA    | 2459 |
| Qy | 1978 | TTGAGAGCCATGCTGGTATATCTCTCTTGCACAGATTTAGCGGAAGAAATCAAACCTTCAG    | 2037 |
| Db | 2460 | CTGAGAGCCATGCTGGTATATACATCTCTTGGCACAGCCTGCGAGAGAAATCAAACCTTCAG   | 2519 |
| Qy | 2038 | AGACTTCTCAGCGAGTTGTAGACACAATCTTATGTCAAAATGTGCAGATGCAATAGCCGC     | 2097 |
| Db | 2520 | AGACTTCTCAGCGAGTTGTAGACACCAATCTTATGAAAGTGCAGACGCGCAATAGCCGC      | 2579 |
| Qy | 2098 | ACAGTCAAGTGTCCATATCAACACTGTTGGAACTGTGCAAGGCCCAAGCAGAGAGAGTTG     | 2157 |
| Db | 2580 | ACGAGTCAGTGTCCATATCAACACTGTTGGAGCTCTGCAAGGGCCCAAGCGGGGAGTTG      | 2639 |
| Qy | 2158 | GCAGTTGGCAGAGAAATPACTTAAAGCTGGATTCATTTGGTATTTGGTGTGTGATTATGTC    | 2217 |
| Db | 2640 | GCAGTTGGCAGAGAAATPACTTAAAGCTGGATTCATTTGGTGTGTGATTATGTC           | 2699 |
| Qy | 2218 | TTAAATTTGTTATCTTTGGAAACCAAACTGAAATCAAACTTTGGCAAGAACTTCTTGGCCGC   | 2277 |
| Db | 2700 | TTAAGTTGTTATCTTTGGAAACCAAGCTGAAATCAAACTTGGCAGAACTCTCTGGGTCG      | 2759 |
| Qy | 2278 | CTTTGCTCTATAGATAGACTGTTGTTGGAAATTTCTGCTGAAATTTTATCTCATATTGTC     | 2337 |
| Db | 2760 | CTCTGCTCTTATAGACAGATTCCTTTGGAAATTTCTGCGAAATTTTATCTCATATTGTC      | 2819 |
| Qy | 2338 | AGTACTGATGTTTCAACAGCTGAGCCCTGTTGAAATCAGGTTATGAAGAGCTGCTGCTCCCTC  | 2397 |







QY 781 GGTGGCAGTGAATCAGAACTCCAGGAGTAGGAGAAAGAGTTTCCCGAGTGCCT 840  
Db 1260 GGGGGCTCAGGGAAGCCGGAATCCCAGGAGTGAGACGGAAAAGAGTGTCCCAGATGCCT 1319  
QY 841 TTTGAGAGTGGCAGAAATCACACACCCCGAAGAGCCCTTCAACAGAGTGCCTTCTCAACA 900  
Db 1320 TTCAGAGTGGCAGAAATCACACCACTCCGAGAGCCCGCTCGCCAGATGCTTCTCACCG 1379  
QY 901 TATAGCCCTGAGGAAACAAACCGCGCTGTGTTAAACAAAGTGATGGGGCCAGACTGTACTTA 960  
Db 1380 TACAGCCAGAGGAGACAGCGCCGCTGTGNAACAAAGTGATGAGGGCCAGGCTGTACTTC 1439  
QY 961 CTGAGCAGATPAGGCGCTAACTCTTTCTGATTTGGAGAGACAGCCAGACAATAATAC 1020  
Db 1440 CTGAGCAGATPAGGACCAACTCTTTCTGATTTGGAGAGACAGTCCAGACAATAATAC 1499  
QY 1021 CGGGTGTTTATTTGGGCTTCAGAACTGCAGCTGTGCAGTGGAACATTTCTGTTTCACTG 1080  
Db 1500 CGCGTGTATTTGGGCCACAGAACTGCAGCTGTGGGCTGGGACATTTCTGCATTCACCTC 1559  
QY 1081 CTATTTGTGATGCTCGGGTGTGTTCAACTAGAACCTTTAGACCCCAATGTTTATGGAGAAA 1140  
Db 1560 TTGTTTGTATGCTCGGGTGTGTTCCAGCTAGAACCTTCGACCCCATGCTATGGAGAAAA 1619  
QY 1141 ACTTTAAGAAATTTGAGTTGAGATTTGTTCCAGAAATATACACAGTAGGCTGAGTCA 1200  
Db 1620 ACTTTAAGAAATTTGAGTTGAGATTTGTTCCAGAAATACACAGTAGGCTGAGTCA 1679  
QY 1201 AGGATCAAGCTCCATCTCGTAACCAATCCAGAAAGTTGTTTCAACGCATGTCAAAATCT 1260  
Db 1680 AGAATCAAGCTCCATCTCGTAACCAATCCAGAAAGTTGTTTCAACGCATGTCAAAATCT 1739  
QY 1261 CATACATTTGATCTAGTACTTCTACGCTGATGTTCCAGAAACACATCAAGGATGAA 1320  
Db 1740 CACACATTTGATCTAGTACTTCTACGCTGATGTTCCAGAAACACATCAAGGATGAA 1799  
QY 1321 GAGAAACAGATGTGCTTATTTGCTTGTGGGCACTGCTTGATGAAGAAAGTCTTTACAGTG 1380  
Db 1800 GAGGACAGATGTGCTTATTTGCTTGTGGGCACTGCTTGATGAAGAAAGTCTTTACAGTG 1859  
QY 1381 TGTGAGACGCTGACAGAAACAGCTGCACCACTGCATGTCATTTGGGACAGAGAG 1440  
Db 1860 TGTGAGACGCTGACAGAAACAGCTGCACCACTGCATGTCATTTGGGACAGAGAG 1919  
QY 1441 TGTGAGAAATAGAGAACTTTAATATGTCCTCTTTGTAGATCTAAGTGGAGATCTCAT 1500  
Db 1920 TGTGAGAAATAGAGAACTTTAATATGTCCTCTTTGTAGATCTAAGTGGAGATCTCAT 1979  
QY 1501 GATTTCTACAGCAGATTTCTAAGTCTGTGATTTCCCTTCTTCCCTCAGAGCTGCA 1560  
Db 1980 GACTTCTACAGCAGATTTCTAAGTCTGTGATTTCCCTTCTTCCCTCAGAGCTGTA 2039  
QY 1561 CAGCAGCAACCGTACAGCAGCAGCTTTGGCTGGATCA---CGAAGAAATCAAGAGAGC 1617  
Db 2040 CAGCAGCCTCTCTCCCGCAACGCTGTGCGCGATCACAGCGGAGGAATCAGAAAGC 2099  
QY 1618 AATTTTAACTTACTCATATTAGAACTCAGCAATCCCTCTGCTTACAAAGATTTAGCT 1677  
Db 2100 AATTTTAACTTACTCATATTAGAACTCAGCAATCCCTCTGCTTACAAAGATTTAGCT 2159  
QY 1678 GAGCCATGATTCAGTCTGTTGGAAATGAACTCGTTGGCTGCTTATTTCTAGAAACTGG 1737  
Db 2160 GAGCCATGATTCAGTCTGTTGGAAATGAACTCGTTGGCTGCTTATTTCTAGAAACTGG 2219  
QY 1738 AATGTGAGAGATGGCCCTCAGGCGTCTTTCCCATGATGATGAGTGGGGCCCTGCTGTTG 1797  
Db 2220 AACGTAAAGGAGATGGCCCTTAGGGCCCTTTCCACGATGTTAGCGGGCCCTGTTGTTG 2279  
QY 1798 GCAATGGGGAGACATGGAATTTCTGGGGCAGCAGTGGAGCAGCCAGTGGGGA 1857  
Db 2280 GCGAAGGGGAGACATGGAATTTCTGGAGCGGCGAGGAGGAGCTTAAGTGTCTGGC 2339  
QY 1858 GCCACCAAGTGGTCTTTCCAGACCACTATCTCAGGAGATGTTGGTGGAGGATGCTGCAGC 1917

Db 2340 GCCCGCAGTGGTCTTCCAGCCAGCATCTCAGGGAGCTGTGTGGAGCGCTTCTGCAGC 2399  
QY 1918 GTTCTGTCAATGGTCTGTGCTGACCCCTGTCTACAAAGTGATGCTGTCTTTTAAABACA 1977  
Db 2400 GTCTGTCTATCGTGTGCGCTGACCCCTGTCTACAAAGTGATGCTGTCTTTTAAABACA 2459  
QY 1978 TTGAGAGCCATGCTGCTGATATATACTCTTTGCCACAGTTTGTAGCGGAAAGAAATCAAACTTCAG 2037  
Db 2460 CTGAGAGCCATGCTGCTGATATACATCTCTTTGCCACAGCTGTGCGAAGAAATCAAACTTCAG 2519  
QY 2038 AGACTTTCTCAGCAGATTTGTAGACACCATCTAGTCAATGTGCAGATGCGCAATAGCCGC 2097  
Db 2520 AGACTTTCTCAGCAGATTTGTAGACACCATCTAGTCAATGTGCAGATGCGCAATAGCCGC 2579  
QY 2098 ACAAGTCAAGCTGTCCATATCAACACTGTTGGAACCTGTGCAAGGCGCAAGCAGGAGAGTTG 2157  
Db 2580 ACGAGTCAAGCTGTCCATATCAACACTGTTGAGCTGTGCAAGGCGCAAGCAGGAGAGTTG 2639  
QY 2158 GAGTTGGCAGAGAAATCTAAAGCTGGATCCATTTGTTATTTGTTGTTGATTTATGTC 2217  
Db 2640 GCAAGTTGACGAGAAATCTTAAAGCTGGATCCATTTGTTGTTGTTGTTGATTTATGTC 2699  
QY 2218 TTAATTTGTTATTTTGGAAACCAAACTGAATCAAACTGAATGCGCAAGAACTTCTTTGGCCGC 2277  
Db 2700 TTAAGTGTATTTCTTGGAAACCAAGCTGAATCAAACTGAATGCGCAAGAACTTCTTTGGCTGC 2759  
QY 2278 CTTTGTCTTATAGATGATGTTGTTGAAATTTCTGCTGAAATTTTATTCCTCATATTTGTC 2337  
Db 2760 CTTCTGCTTATAGACAGATTTGCTTTGAAATTTCTGCGGAATTTTATTCCTCATATTTGTC 2819  
QY 2338 AGTACTGATGTTTCAAGAGCTGAGCTGTGAAATCAGGTATAGAAAGCTGCTGTCCCTC 2397  
Db 2820 AGTACGATGCTCAAGCCGAGCTGTTGAATCAGGTATAGAAAGCTGCTGTCCCTC 2879  
QY 2398 TTAACTTTGCTTTGCTGATGATTAATTTCCCACTCAATGTTGGCAAACTTTCCAGA 2457  
Db 2880 TTAGCCTTTGCTTTGCTGATTTGCAATTTCCCACTCTATGTTGGCGGAACTCTCGGG 2939  
QY 2458 AGGATCTACTGAGTCTTCAAGAAATGTTACTACAGTACCCCTGTTTCAAAAATG 2517  
Db 2940 AGGATTTATCTGAGCTCAGCAGAAATGTTGACCAAGTCCCTGTTTCCAAAGCTG 2999  
QY 2518 TTAGAAATGCTGAGTGTTCAGTTTCCAGTTTCCACTCACTTCCAGAGTGTGCTGCGGTTGATG 2577  
Db 3000 GTAAACATGCTAAGTGTCTTGGATCTCTCCACTTCCGCGAGATGCGCGCGCTGTGATG 3059  
QY 2578 GCTATTGAGATGAGTGGAAATTCGCAAGCCATCCAGTTGGCGGTAGAAACACTTTG 2637  
Db 3060 GCAATTGACAGAGATGAGAAATTTCCAGGTCTCAGCTGGTTCGGAAGACACTTTG 3119  
QY 2638 GATGCTCAACAGGACAGCTTCTTGAGGATCTGTTTCCAACTATCTGGAACCAACA 2697  
Db 3120 GATGGCCAGCAGACAG---CTCGCAGGCAATTTGGCCCTTCCCGCTATC-----CA 3167  
QY 2698 GAGAACAGTTCCCTGAGTGGACAGCTCCATTTAGAGAAACTTGAAGAGGATTTATGCT 2757  
Db 3168 GAGAGAGCTCCCTTGTAGCAGACAGCCCATGTAGAGAAACTTGAAGAGGATTTAAAGCT 3227  
QY 2758 ACAAAATGAGTCCAGTTTCAAGAGCAATTTGTAGAGACTGGCCAGCAATTTCAATAG 2817  
Db 3228 ACGAGACTGAGTCCAGCTCAGAGGACATTTCTGACAGACTGGCTGGCGTTTCTGTAGGA 3287  
QY 2818 CCTTCTAGTTCAACAAACAAACAACAACAGAGCAACCAAGCCATGTTCAA 2877  
Db 3288 CTTCTCTAGTTCA-----GCAACAAAGAAACCAAGCCACAGTTCAA 3332  
QY 2878 ACAAAAGGAGAGCCCCACAGTCAAGTGTGTTGAACTCCTCTCTTTTATCTCATCATTTCCAA 2937  
Db 3333 ACAAAAGGAGAGCCCCACAGTCAAGTGTGTTGAACTCCTCTCTCTCTCTCTCTCTCTCT 3389  
QY 2938 TTAATGTTTCCAGCTTGTCAACCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2997

|    |      |                                                                   |      |
|----|------|-------------------------------------------------------------------|------|
| Db | 3390 | TTAATGTTTCCAGCAATATACAGCCCAATGTTTCACTCTCCGCCGCTGTCTCCACGAGTGGCTCT | 3444 |
| Qy | 2998 | GCAACAGATGTCTTAAGCATAGACTTTCAGGGATTCATTCCTTCGCAAAATACCTTCTGCA     | 3057 |
| Db | 3450 | GTAACAGATGCTTCTAAGCATAGACCTTCGGCGCGTTTGTTCCTCTGTAATAATACCTCTGG    | 3509 |
| Qy | 3058 | TCTCCTCAAAACAGACGCCAAAGTTTCTCTACAATTCACAGAAACTGTCTCGTGAACAA       | 3117 |
| Db | 3510 | TCTCCCCAACAACAGCGCAAGTTTCCCTACAGTTCAGAGAGACCTGTCTTGAAACCGA        | 3569 |
| Qy | 3118 | GACTCAGATAAACCTTTCCCCAGTCTTTTACTCAGTCAAGAACCCTTGGCCCTCCAGTAACATA  | 3177 |
| Db | 3570 | GACTCAGAAAACCTCTCCCCAGTCTTTTACTCAGTTCGAGACCCCCACCTCCAGTAACATA     | 3629 |
| Qy | 3178 | CACAGGCCAAAGCCCATCTAGACCTTACCCCAAGTAAATAACAAGTAAACAGGAGAGATCCCTCA | 3237 |
| Db | 3630 | CACAGGCCAAAGCCCATCCGACCCGTTCCGGGTAGCACAGCAAACTAGGGGATGCCTCA       | 3689 |
| Qy | 3238 | AAAAATAGCATGACACTTGTCTGAAACAGTAGTTTCAAATGTGATGACAGCTTTGGCTGT      | 3297 |
| Db | 3690 | AAAAACAGCATGACACTCGACCTGAAACAGTGTCTTCCCAAGTGTGATGACAGCTTTGGCAGT   | 3749 |
| Qy | 3298 | AGCAGCAATAGTAGTAATGTGTCTATACCCAGTGACGAGACAGTGTTCACCCCAAGTAGAG     | 3357 |
| Db | 3750 | GGCAGCAACAGTGCAGCGCGTCTATACCCAGTGAGGAGACGGCAITTCACCCAGCAGAG       | 3809 |
| Qy | 3358 | GAGAAATGCAGATTAGATGTCAATACAGAGCTCAACTCCAGTATTGAGGACCTTCTTGAA      | 3417 |
| Db | 3810 | GACAAGTGCAGTTTAGATGTCAACCCCGAGCTCAACTCCAGTATCGAGGACCTTCTTGAA      | 3869 |
| Qy | 3418 | GCATCTATGCCCTTCAAAGTGATACAAACAGTAACTTTTAAAGTCAGAAGTTGTGTCTGTCT    | 3477 |
| Db | 3870 | GCATCTATGCCCTTCAAAGTGACACAAACAGTCACTTTCAAGTCCGAAGTCGCGCTCTCT      | 3929 |
| Qy | 3478 | CCTGAAAAGGCTGAATATGATGATACCTACAAAGATGATGTGATCATATATCAAAAGTGC      | 3537 |
| Db | 3930 | CCTGAGAAGGCCGAAGATGATGACACCTTACAAAGATGACGTCAATCAATCAAAAGTGC       | 3989 |
| Qy | 3538 | AAAGAGAAGATGGAAGCTGGAAGAAGAAGAAGCTTTAGCAATGTCATGGCAATGTCCAGCG     | 3597 |
| Db | 3990 | AAAGAGAAGATGGAAGCTGGAAGAAGAAGGAGGCGCTCGCGATTGCCATGGCAATGTCCGGCT   | 4049 |
| Qy | 3598 | TCTCAGATGCGCTTCCCATAGTTTCTCAGCTGCAGGTTGAAATGAGAGAGATATCATC        | 3657 |
| Db | 4050 | TCTCAGGACGCGCTTCCCATAGTCCCTCAGCTGCAGGTGGAATGAGAGGATATCATC         | 4109 |
| Qy | 3658 | ATTATTCAACAGGATACACCAAGAGACTTACCCAGGACATACCAAGCAAAACCAACCGTAT     | 3717 |
| Db | 4110 | ATCATCCAGCAGSATACACCAAGAAACCCATACCGGCGCATCCAAGCGAACGAGCCCTAC      | 4169 |
| Qy | 3718 | AGAGAGACCTGATGCTGAAAGGTCAACAGATAGCCCTTGAGACATTTCTTCTGT            | 3777 |
| Db | 4170 | AGAGAAGACACCGATGCTGAAAGGGCAGCAGATAGCCCTCGGAGGATTTTCTTCTGT         | 4229 |
| Qy | 3778 | TATCAGGCTCAAGATGTGGGAACCTGGAACITTAATGGCTGTAAACAGGTGACTTATGTC      | 3837 |
| Db | 4230 | TACCAAGCACAGGATGTGGGCACTGGAACITTAATGGCTGTGAAACAGGTGACCTACGTC      | 4289 |
| Qy | 3838 | AGAACACATCTCTGACGACGACGAGTACTAGACACATTAAGAGAGAGATAGAGATG          | 3897 |
| Db | 4290 | AGAAACACATCTTCTGACGACGAGAGTGTGGAGCCCTTGAGGGAGAGATCAGGATG          | 4349 |
| Qy | 3898 | ATGAGCCATCTGAAATCATCCAAACATCATATTAGGATGTTGGGAGGCCAGTGTGAGAAGGC    | 3957 |
| Db | 4350 | ATGAGCCACCTCAACCATCCGAAACATCATCAGGATGCTGGGGGCCACGTCGAGAAGAC       | 4409 |
| Qy | 3958 | AATTACATCTCTTCATTTGAATGATGCGAGGGGATCGGTGGCTCATTTTCTCAGTAAA        | 4017 |
| Db | 4410 | AACATAAACCTCTTCATCGATGATGCGGGAGCCTCCGTGGCTCACTCTTGAGTAAA          | 4469 |
| Qy | 4018 | TATGAGCCTTCAAAAGATACGATAGTTATTAACATACACTGAACAGTACTCCGTGGCCTT      | 4077 |
| Db | 4470 | TATGAGCTTCAAGGAGCTAGTGTGATTAACATACAGAGCAGTACTCCGTGGCCTT           | 4529 |

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| Qy | 4078 | TCGTAATCTCCATGAAACCAAAATCAATTCACAGAGATGTCAAAGCGTGCCAAATTTGCTAAATT | 41337 |
| Db | 4530 | TCCTATCTCCACGAGAACCAATCATTTCAACAGAGACGTCAAAGGGGCGCAATCTGCTCAATT   | 4589  |
| Qy | 4138 | GACAGCACTGGTCAGAGACTAAGAAATTCAGATTTTGGAGCTCGAGCCAGGTTGGCATCA      | 4197  |
| Db | 4590 | GACAGCACCGGTACGCGCTCAGAAATTCAGAGACTTCGGTCTCGCCGCCAGGTTGGCATCC     | 4649  |
| Qy | 4198 | AAAGGAACCTGGTCAGAGAGAGTTTCAGGGHCAATTTACTGGGGHCAATTTGCAATTTATGGCA  | 4257  |
| Db | 4650 | AAAGGAACCTGGTCAGAGAGAGTTTCCAGGGHCAAGTTACTGGGGHCAATTTGCAATTCAGGGC  | 4709  |
| Qy | 4258 | CCTGAGGTACTTAAGAGGTCAACAGTAGTGAAGAGAGCTGTGATGTATGGAGCTGTGTGGCTGT  | 4317  |
| Db | 4710 | CCTGAGGTACTTAAGAGGTCAAGAGTAGTGAAGAGCTGTGAGCTGTGGAGTGTGTGGCTGC     | 4769  |
| Qy | 4318 | GCTATTAGAAATGGCTTGTGCAAAACCAACCATGGAAATGCAGAAAAACAACCTCAATCAT     | 4377  |
| Db | 4770 | GCCATTATAGAAATGGCTGTGCAAAACCAACCATGGAAACGAGAAAAAGCACTCCAATCAT     | 4829  |
| Qy | 4378 | CTTGCTTTGATATTAGATTTGCTAGTGCACTACTGCTCCATCGATCCCTTCACATTTG        | 4437  |
| Db | 4830 | CTTGCTTTGATATTAGATTTGAGTTGGAGTGCAGTACTGCACTCATCCATCCCGTCAACCTG    | 4889  |
| Qy | 4438 | TCTCCTCGTTTACGAGATGGCTCTTTCGTTTGTTTAGAACTTCAACCTCAGGACAGACCT      | 4497  |
| Db | 4890 | TCCCGGGGCGCTCGAGACGTTGGCTCTCGCGCTGTTTAGAACTTCAACCTCAGGACAGACCT    | 4949  |
| Qy | 4498 | CCATCAAGAGAGCTACTGAAGCATCCAGTCTTTTCGTACTACATGGTAGCCAAATTTATCGAG   | 4557  |
| Db | 4950 | CCGTCAAGAGAGAGCTACTGAAGCATCCCTGTCTTCGTACAAACATGGTAGTCAACT- ----   | 5003  |
| Qy | 4558 | ATCAACTACAGTAGAAGAACAGGATGCTCAACAAAGAGAAAAAACTTCTGGGGAACCCACAT    | 4617  |
| Db | 5004 | -----GCTCAGGGTGGCGCAACAAG-GAAGAAAACTTCGCGGGCAGCCACGT              | 5048  |
| Qy | 4618 | TGATATTCTACTGGCCATGATGCCACTGAACAGCTATTGAACGAGGCCAGGTGGGGAAACCCCT  | 4677  |
| Db | 5049 | TGATAGTCTGTGGCC-TCATACCACCTGACCAG----AAGAGGGGGCAGGTGGGGAGCCCG     | 5103  |
| Qy | 4678 | TACCTTAGTATGTGATTGACAAATCATGATCTGTACCTTAAGCTCAGTATGCAAAAGGCCCA    | 4737  |
| Db | 5104 | CACCTTAGCATGTGACTGACAAATCATGA-CTGCACCTGAGCTCCGTCTGCAGACGGCTA      | 5162  |
| Qy | 4738 | -AACTAGTGCAGAAACTG                                                | 4754  |
| Db | 5163 | CAACTCGTGCAAGGAGCTG                                               | 5180  |

RESULT 10

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ID AAX80911 standard; cDNA; 5253 BP.

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| DT | 03-NOV-1999 | (first entry)                                                           |
| XX |             |                                                                         |
| DE |             |                                                                         |
| XX |             |                                                                         |
| XX |             | Murine MEK1 cDNA.                                                       |
| KW |             | Murine MEK1 cDNA; Mitogen ERK Kinase 1 protein; MEK1; protease          |
| KW |             | extracellular signal regulated kinase; ERK; signal transduction pathway |
| KW |             | regulation; apoptosis; protein kinase; cleavage; casease; antibody;     |
| KW |             | kinase fragment; mutant MEK1 protein; NH2-terminal fragment; detection  |
| KW |             | immunoreactive; diagnostic; therapeutic assay; reagent; disorder;       |
| KW |             | aberrant expression; activation; MEK1 gene product; DNA probe; primer;  |
| KW |             | selectively hybridize; ss.                                              |

XX

OS Mus sp.



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QY 1426 ATTTGGGCAGAGAGTGTAGAGAAATAGAGAACTTTAATATGTGCTCCCTTTGTAGATCT 1485  
DB 1419 ATCTGGCGGAGAGTGTAGAGAAATAGAGAGCTTTAATATGTGCTCCCTTTGTAGATCT 1478  
QY 1486 AAGTGGAGATCTCATGATTTCTACAGCAGAGTGTCAAGTCTGTGGATTCCTCTCT 1545  
DB 1479 AAGTGGAGATCCCATGATCTCTACAGCCATGAGTTATCAAGCCCGGTGGAGTCCCGGCC 1538  
QY 1546 TCCCTCAGAGCTGACAGCAGCAACCGGTACAGCAGCAGCTTTGGCTGGATCA--CGA 1602  
DB 1539 TCCCTGGAGCTGTCCAGCAGCCATCTCTCCCGCAGCAGCCGCTGGCGGATCACAGCGG 1598  
QY 1603 AGGAATCAAGAGAGCAATTTTAACCTTACTCATTTATGGAATCAGCAATTCCTCTGCT 1662  
DB 1599 AGGAATCAGGAGAGCAGTTTAACTTACTCATTTTGGAAACCCAGCAGATTCCTTCGCT 1658  
QY 1663 TACAAAGATTTAGCTGAGCCATGATTCAGTGTGTTGGAAATGGAATTCGTTGGCTGCTTA 1722  
DB 1659 TACAAAGATTTGGCCGAGCCATGATTCAGTGTGTTGGAAATGGAATTCGTTGGCTGCTTA 1718  
QY 1723 TTTTCTAGAACTGGAATGTGAGAGAGATGGCCCTCAGGGCTCTTCCCATGATGTGAGT 1782  
DB 1719 TTCTTAGAACTGGAAGCTAAGGGAATGGCCCTTAGGGCTCTTCCCAAGCAGCTTAGT 1778  
QY 1783 GGGCCCTGCTGTTGGCAATGGGAGAGCACTCGAAATCTGGGGGCAGCAGTGGAGC 1842  
DB 1779 GGGCCCTGTTTGGCAACGGGAGAGCACTGGAACTCTGGAGCGGCAGTGGGGC 1838  
QY 1843 AGCCGAGTGGGAGGACACAGTGGGTCTTCCAGACCAATGATCTCAGGAGATGTGGTG 1902  
DB 1839 AGCTTAAAGCGGGAGCGGCAGCGGGTCTTCCAGGCCAGCATCTCAGGGGATGTGGTG 1898  
QY 1903 GAGCATGCTCAGCGTCTCTCAATGTCTGCTGCTGACCTGCTGTACAAAGTGTAGCTT 1962  
DB 1899 GAGCGTCTCAGTGTCTCTGTCTATAGTCTGCGCTGACCTGCTGTACAAAGTGTAGCTT 1958  
QY 1963 GCTGCTTTAAAAACATTAGAGCCATGCTGTATATATCTGCTGCCACAGTTAGCGGAA 2022  
DB 1959 GCTGCTTTAAAAACATTAGAGCCATGCTGTGTAATACACTCTTGCCACAGTCTGGCAGAA 2018  
QY 2023 AGAATCAACTCAGAGCTCTCCAGCGCTGTAGACCACTCTAGTCAATGTGCA 2082  
DB 2019 AGAATCAACTCAGAGCTCTCCAGCGCTGTAGACACTATCTTGTCAAGTGTGCA 2078  
QY 2083 GATGCCAATAGCCGACAAAGTCACTGTCCATATCAACACTGTTTGGAACTGTGCAAGGC 2142  
DB 2079 GATGCCAAGCCGACAGTCACTGTCCATATCTACAGTGTGGAACCTCTGCAAGGC 2138  
QY 2143 CAAGCAGAGAGTGGCAGTGGCAGAGAAATACATAAGCTGATCCATGTTGTTGGT 2202  
DB 2139 CAAGCAGAGAGTGGCGGTTGGGAGAGAAATATCTTAAAGCTGGGTCCATCGGGGTTGGT 2198  
QY 2203 GGTGTTGATTATGCTTAAATGTTATCTTGGAAACCAAACTGAATCAAACTGGCAA 2262  
DB 2199 GGTGTCGATTACGCTTAAAGTGTATCTTGGAAACCAAGCTGAATCAAACTGGCAA 2258  
QY 2263 GAATCTTGTGGCGCTTGTCTATAGATAGACTGTGTTGGAAATTCCTGCTGAAATTT 2322  
DB 2259 GAATCTGTGGTGTGCTGTCTATAGACAGGTTGCTGTTGGAAATTCCTGCTGAAATTC 2318  
QY 2323 TATCCTCATATTTGTCAGTACTGATGTTTCAAGCTGAGCCTGTTGAAATCAGGTATAAG 2382  
DB 2319 TATCCTCATATTTGTCAGTACTGATGTTTCAAGCTGAGCCTGTTGAAATCAGGTATAAG 2378  
QY 2383 AAGCTGTGCTCCTTTAACTTTGCTTTGAGTCCATGATTAATTCCTCAATGTT 2442  
DB 2379 AAGCTGTGCTCCTTTAACTTTGCTTTGAAATTCATTTGCAATTCCTCAATGTT 2438  
QY 2443 GGCACACTTCCAGAGAGATCTACTTGTGATCTGCAAGATGGTTTACTTACAGTACCCCAT 2502  
DB 2439 GGCACACTCTCTCGAGAGATATATCTGAGCTCTGCGAGATGGTGACCGCAGTCCCGCT 2498  
QY 2503 GTGTTTTCAAACTGTTAGAAATGCTGAGTGTGTTTCCAGTTCCTCACTTCCAGGATG 2562

DB 2499 GTGTTTTCAAGCTGGTAACCATGCTTAAATGCTTCTGGCTCCACCACTTCCACAGGATG 2558  
QY 2563 CGTCCCGCTTTGATGCTTATTCGATCAGGTGGAAATTCGCGAGCCATCCAGTTGGC 2622  
DB 2559 CCGCGGCTGTGATGCTTATCGCGATGAGGTAGAAATTCGCGAGTCACTCCAGCTGGT 2618  
QY 2623 GTAGAGACACTTTGGATGGTCAACAGGACAGCTTCTTTCAGGCACTGTGTTCCCAACAC 2682  
DB 2619 GTGAGGACACTGTGATGGGCTATCAGGACAG--CTTACAGCGCGTGGCCCCCAGCAGC 2675  
QY 2683 TATCTGGAAACACAGAGAACTGCTTCCCTGAGTGCACAGTCCATTTAGAGAAACTGGA 2742  
DB 2676 TGTCT-----AGAAACAGCTCTTCTGAGCACTAGTCCATGAGAGAAACTGGA 2726  
QY 2743 AAAGGATATTGTGTACAAAATGAGTCCAGTTCAGAGGACATTTCTGAGAGACTGGCC 2802  
DB 2727 AAAGGACTAAGTGTCTACGAGCTGAGTCCAGCTCGAGGACATTTCTGAGAGACTGGCC 2786  
QY 2803 AGCATTTCACTAGTACCTTCTAGTTCAACAAACAAACAAACAGAGCAACCA 2862  
DB 2787 GCGCTCTCTGTAGGACTTCCCAGCT-----CAACAAACAGAGCAACCA 2831  
QY 2863 AAGCAATGCTTCAAAACAAAGGAGAGCCCAACAGTCACTGAGTGTGAACTCTCTCTTTA 2922  
DB 2832 AAGCCAGCGTTTCAAAACAAAGGAGAGCCCAACAGTCACTGAGTGTGAACTCTCTCTTTG 2891  
QY 2923 TCTCATCTTCCCAATTAATGTTCCAGCTTGTCAACCGCTTCTTCTTACCCCATCT 2982  
DB 2892 TC---TCATGCTCAATTAATGTTTCCAGCAGCATCAGCCCTTGTCTCTGCCCCGCT 2948  
QY 2983 GTACCAGCTGGCAGCTGCAACAGATGCTCTTAAGCATAGACTTCAGGGATTCATTTCCCTGC 3042  
DB 2949 GTCC-----CAGATATTTCTAAGCAGAGCCAGGCTTTGTTCCCTGC 2993  
QY 3043 AGAATACCTTCTGATCTCTCTCAACAGAGCGAGTGTCTCTACAAATTCACAGAAAC 3102  
DB 2994 AATATACCTTCCGCTCTCTCAGACAGCGCAAGTCTCTCTCAAAATTCAGAGGAC 3053  
QY 3103 TGTCTGAAACAAAGACTCAGATAAATTTCCCAAGCTTCTTACTCAGTCAAGACCTGTG 3162  
DB 3054 TGCTCTGAACACGAGACTCAGACCAGCTCTCCAGCTCTTCTCAGTCAAGACCCCA 3113  
QY 3163 CCTCCAGTAAATACACAGGCCAAAGCCATCTAGACCTACCCAGGTAAATACAGTAA 3222  
DB 3114 CCTCCAGTAAATACACAGGCCAAAGCCATCCCGACCTCCCGGCGAGTACAGAGCAA 3173  
QY 3223 CAGGAGATCTCTCAAAATAGCATGACATGATCTGAACAGTAGTTCCAAATGTGAT 3282  
DB 3174 CTAGGGAGCCACAAAGTAGTAGCATGATGATCTTGGCAGTGTCTTCCAGGTGTGAC 3233  
QY 3283 GACAGCTTTGGCTGTAGCAGCAATAGTAGTAATGCTGTTATACCAGTGAACAGAGTGTG 3342  
DB 3234 GACAGCTTTGGCGCGCGGCAACAGTGGCAACGCGCTCATACCAGGAGCAGAGAGTGTG 3293  
QY 3343 TTCACCCAGTGAAGAGAAATGCGAGTGTAGATGTCAATACAGAGTCAACTCCAGTAT 3402  
DB 3294 TTCACCCGCTGGAGCAAGTGAAGTGTAGATGTGAACACAGAGTCAACTCCAGCATC 3353  
QY 3403 GAGGACTCTTTCAGAGCATCTATGCTTCAAGTGTATCAACAGTAACTTTTAAAGTCAGAA 3462  
DB 3354 GAGGACTCTTTCAGAGCATCTATGCTTCAAGTGTATCAACAGTCACTTTCAAGTCCGAA 3413  
QY 3463 GTTGTCTCTCTCTCTGAAAGCTGAAATGATGATACCTCAAGATGATGTGAT 3522  
DB 3414 GTCCGCTCTCTCTCGGAAAGGCGGAAATGACACCTTCAAGAGAGAGGCTTTCAGCATC 3473  
QY 3523 CATAAATCAAAAGTGAAGAGAGATGGAAGCTGAAGAGAGAGAGCTTTTACCAATGTC 3582  
DB 3474 CATAAATCAAAAGTGAAGAGATGGAAGCTGAAGAGAGAGAGGCTTTTACGATCGCC 3533  
QY 3583 ATGGCAATGTGAGCTCTCAGGATGCCCTCCCATAGTTCCTCAGCTGAGGTGAAT 3642



Db 3534 ATGGCGATGTTCAGGCTCTCAGGATGCCCTCCCATCGTCCCTCAGCTGCAGGTGGAAAT 3593  
Qy 3643 GGAGAAGATATCATATTATTAACAGGATACACAGAGACTCTTACACAGACATACCCAA 3702  
Db 3594 GGAGAAGATATATCATATTATTAACAGGATACACAGAGACTCTTACACAGACATACCCAA 3653  
Qy 3703 GCAAAACACCGTATAGAGAGAGACATGAAATGGCTGAAAGGTCAACAGATAGGCTTTGGA 3762  
Db 3654 GCGAAACACCGCTTACAGAGAGAGCGCTGAGTGGCTGAAAGGCCACAGCAGATAGGCTCGGA 3713  
Qy 3763 GCATTTCTCTCTGTATATCAGGCTCAAGATGTGGAACTGGAATCTTTAATGGCTGTAAA 3822  
Db 3714 GCATTTCTCTCTGTATATCAGGCTCAAGATGTGGAACTGGAATCTTTAATGGCTGTAAA 3773  
Qy 3823 CAGGTGATATATGTCAGAAAACATCTTCTTCTGAGCAAGAGAGTATGTAAGACATAGA 3882  
Db 3774 CAGGTGATATATGTCAGAAAACATCTTCTTCTGAGCAAGAGAGTATGTAAGACATAGA 3833  
Qy 3883 GAAGAGATAGAGATGATGAGCCATCTGAATCATCCAAACATCATTTAGGATGTTGGGAGCC 3942  
Db 3834 GAAGAGATCCGATGATGGGTCACTCAACCATCAAAACATCATCCGATGCTGGGGGCC 3893  
Qy 3943 ACGTGTGAGAGAGCAATTAACAATCTTCTTCTTCAATGATGGATGGAGGGGATCGTGGCT 4002  
Db 3894 ACGTGTGAGAGAGCAATTAACAATCTTCTTCTTCAATGATGGATGGAGGGGATCGTGGCT 3953  
Qy 4003 CATTTGCTGATTAATATGAGGCTTCAAGAAATCAGTATGTTATTAATCACTACAGACAG 4062  
Db 3954 CACCTCTTGATTAATATGAGGCTTCAAGAAATCAGTATGTTATTAATCACTACAGACAG 4013  
Qy 4063 TTACTCCGTGGCTTTCGTATCTCCATGAAGAAACCAATCAATTCACAGAGATGTCAAAAGT 4122  
Db 4014 TTACTCCGTGGCTTTCGTATCTCCATGAAGAAACCAATCAATTCACAGAGATGTCAAAAGT 4073  
Qy 4123 GCCATTTGCTTAATATGAGGCTTCAAGAAATCAGTATGTTATTAATCACTACAGACAG 4182  
Db 4074 GCCAATCTGCTCAATGAGCAGACCGGTGAGAGGTGAGAAATGAGAGCTTTGGAGCTGCT 4133  
Qy 4183 GCCAGGTGGCATCAAAAGGAACTGGTGCAGAGAGATTTTCAGGACCAATTAATCTGGGACA 4242  
Db 4134 GCCAGGTGGCATCAAAAGGAACTGGTGCAGAGAGATTTTCAGGACCAATTAATCTGGGACA 4193  
Qy 4243 ATTGATTTATGGCACTGAGGTACTAAGAGTCAACAGTATGGAAGAGCTGTGATGA 4302  
Db 4194 ATTGATTTATGGCACTGAGGTACTAAGAGTCAACAGTATGGAAGAGCTGTGATGA 4253  
Qy 4303 TGGAGTGTGGCTGTCTTATTAAGAAATGGCTTGTCAAAACCAACCATGGAATGCAGAA 4362  
Db 4254 TGGAGTGTGGCTGTCTTATTAAGAAATGGCTTGTCAAAACCAACCATGGAATGCAGAA 4313  
Qy 4363 AAACATCAATCATCTTCTTGTATTTAAGATGCTAGTGCATCTACTGCTCCATCG 4422  
Db 4314 AAACATCAATCATCTTCTTGTATTTAAGATGCTAGTGCATCTACTGCTCCATCG 4373  
Qy 4423 ATCCCTTCACTTGTCTCTCTGTATTAAGATGCTAGTGCATCTACTGCTCCATCG 4482  
Db 4374 ATCCCTTCACTTGTCTCTCTGTATTAAGATGCTAGTGCATCTACTGCTCCATCG 4433  
Qy 4483 CTTGAGGACAGACCTTCCATCAAGAGAGCTACTGGAAGCATCCAGTCTTTCGTACTACATGG 4542  
Db 4434 CTTGAGGACAGACCTTCCATCAAGAGAGCTACTGGAAGCATCCAGTCTTTCGTACTACATGG 4493  
Qy 4543 TAGCCAAATATGAGATCAACTACAGTACAGAAACAGGATGCTCAACAGAGAAAGAAACT 4602  
Db 4494 TAGTTAATTTGCTCAGTCTCTATGAGACAGGATATGCAACCGGAGAGAGAAAG 4553  
Qy 4603 TG----TGGGAAACCAATGATATTTCTACTGGCATGATGCCATGACAGTATGAAC 4658  
Db 4554 AGAACTTGTGGGCGACCATGCGCTAAACCGCAGCCCTCACGCCACTGAACAGCCAGAAAC 4613  
Qy 4659 GAGGCGAGTGGGAAACCTTACTAGTATGATGATGATGATGATGATGATGATGATGATGATG 4718  
Db 4614 GGGGCCAGCGGGGAA--CGGTACTAGCATGTGATTTGACAAATATGACCTGTACTTANG 4672

Qy 4719 CTCAGTATGCA-AAAGCCCAAACTAGTGCAGAAACTGTAAACTGTGCTTCAAGAACT 4777  
Db 4673 CTCGATATGCAGACATCTACAGCTCGTGCAGAACTGCACACCGTGCCTTTACAGGACT 4732  
Qy 4778 GCGCCCTAGTGTACAGGAAACAAATGAAGTTTGCATGACTAAATTTGCGAGAGCAATTT 4837  
Db 4733 GCGCTCTGGGGACCAAGGAGCGATGGAGTTTGCATGACTAAAGAACAGAGCATAAAT 4792  
Qy 4838 TATTTTTTTGGAGCACTTTTTTTCAGCAA 4864  
Db 4793 TA--TTTTTGGAGCACTTTTTTTCAGCTA 4817

## RESULT 11

AAZ25072

ID AAZ25072 standard; cdNA; 5253 BP.

XX

AC AAZ25072;

XX

DT 09-DEC-1999 (first entry)

XX

DE Murine MEK1 nucleotide sequence.

XX

KW MEK1; MEK2; MEK3; mitogen-activated protein kinase; MAPK; ERK;  
extracellular regulated kinase; signal transduction; regulation;  
KW MAPK/ERK; MEK; MKK; inflammation; cellular proliferation;  
KW differentiation; development; cell death; ss.

XX

OS Mus musculus.

XX

FH Key

CDS Location/Qualifiers

FT 15..4496

FT /\*tag= a

FT /product= "MEK1"

XX

XX WO9947686-A2.

XX

XX 23-SEP-1999.

XX

XX 15-MAR-1999; 99WO-US005556.

XX

XX 16-MAR-1998; 98US-0078153P.

XX

XX 04-SEP-1998; 98US-0099165P.

XX

XX (CADU-) CADUS PHARM CORP.

XX

XX Johnson GL;

XX

XX WPI; 1999-571843/48.

XX

XX P-PSDB; AAY42107.

XX

XX New human MEK1 polynucleotides and polypeptides, used for regulating  
signal transduction in cells.

XX

XX Example 1; Fig 3; 159pp; English.

XX

XX The present sequence encodes murine mitogen-activated protein kinase/  
extracellular responses kinase (MAPK/ERK) kinase kinase (MEKK),  
specifically designated MEKK1. The MEKK proteins are used to modulate and  
regulate signal transduction in cells, as well as for regulation of gene  
expression in a cell encoding MEKK, where the cell is involved in  
inflammation, regulation of cellular proliferation and differentiation,  
regulation of development, regulation of cell death or regulation of  
inflammation. They are also used to prepare antibodies. MEKK  
polynucleotides can be used to produce the protein recombinantly and as a  
source of probes and primers

XX

SQ Sequence 5253 BP; 1299 A; 1403 C; 1433 G; 1118 T; 0 U; 0 Other;

XX

XX Query Match

XX Best Local Similarity 65.1%; Score 3417; DB 2; Length 5253;

XX Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;

QY 1 GAGAAATGGCGGCGGCGGGAATCGCGCTCGTCTCGGATTCGCGGCGCGCAGG 60  
Db 9 GAGAAATGGCGGCGGCGGCGGATCGCGCTCGTCTCGGATTCGCGGCGCGCAGG 68  
QY 61 GCTACGAGCCTCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 111  
Db 69 GCGGAGTCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 128  
QY 112 GCGGCC---GCGGCTGCGCGGAGTCTGCGGAGCGGCGGCGGCGGCGGCGGCGG 168  
Db 129 GCGGCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 188  
QY 169 GCGGACTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 228  
Db 189 GCGGACTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 248  
QY 229 GAGCAGCGGCTTCCTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 285  
Db 249 GAGCAGCGGCTTCCTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 308  
QY 286 GAGCCCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 345  
Db 309 GAGCCCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 368  
QY 346 CACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 405  
Db 369 CCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 428  
QY 406 GCGGCTCGAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 465  
Db 429 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 458  
QY 466 TCTCTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 525  
Db 459 CCCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 518  
QY 526 CACGAGTGTATGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 585  
Db 519 CACGAGTGTATGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 578  
QY 586 ATGCGAGCTGGAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 645  
Db 579 ATGCGGCTGGAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 638  
QY 646 AAACCAATCCAGTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 705  
Db 639 AAGCAATCCCTATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 698  
QY 706 GAGAGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 765  
Db 699 GAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 758  
QY 766 GCGAATCCCGATCAGGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 825  
Db 759 GCGAGCTCCGTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 818  
QY 826 GTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 885  
Db 819 GTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 878  
QY 886 GATGCTTCTCACCATAGCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 945  
Db 879 GATGCTTCTCCCGTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 938  
QY 946 GCGAGCTGTACTTACTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1005  
Db 939 GCGAGGCTGTACTTACTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 988  
QY 1006 CCAGCAATAAATACCGGCTGTTATGCGGCTCAGAACTGCACTGTGACGCTGGAACA 1065  
Db 999 CCAGCAATAAATACCGGCTGTTATGCGGCTCAGAACTGCACTGTGCGGCTGGAGCA 1058

QY 1066 TTCTGTATTCACTGCTATTTTGTGATGCTCGGGTGTTCACCTAGACCTTCAGACCA 1125  
Db 1059 TTCTGTATTCACTGCTATTTTGTGATGCTCGGGTGTTCACCTAGACCTTCAGACCA 1118  
QY 1126 ATGTTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1185  
Db 1119 ATGTTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1178  
QY 1186 AGTAGCGTGTCTAAGGATCAAGCTCCATCTCGTAAACACATCCAGAGGAGGAGG 1245  
Db 1179 AGTAGCGTGTCTAAGGATCAAGCTCCATCCCGGAGGAGGAGGAGGAGGAGGAGG 1238  
QY 1246 CCGATGTCAAAATCTCTACATCTGTCTACATCTGTCTAGCTCTAGCTCTAGCTCT 1305  
Db 1239 CCGATGTCAAAATCTCTACATCTGTCTACATCTGTCTAGCTCTAGCTCTAGCTCT 1298  
QY 1306 AGCTAAAGGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1365  
Db 1299 AGCTAAAGGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1358  
QY 1366 GAAAGTCTTACAGTGTGTGAAGCGGCTGCAGGAGGAGGAGGAGGAGGAGGAGGAG 1425  
Db 1359 GAGAGCTGTACTGTGTGAAGTGGCTGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 1418  
QY 1426 ATTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1485  
Db 1419 ATCTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1478  
QY 1486 AAGTGGAGATCTCATGATTTCTACAGCCAGGAGGAGGAGGAGGAGGAGGAGGAG 1545  
Db 1479 AAGTGGAGATCCCATGATTTCTACAGCCAGGAGGAGGAGGAGGAGGAGGAGGAG 1538  
QY 1546 TCCCTCAGAGTGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1602  
Db 1539 TCCCTCAGAGTGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1598  
QY 1603 AGGAATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1662  
Db 1599 AGGAATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1658  
QY 1663 TACAAGATTTAGCTGAGCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1722  
Db 1659 TACAAGATTTAGCTGAGCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1718  
QY 1723 TTTTCTAGAACTGGAATGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1782  
Db 1719 TTTTCTAGAACTGGAATGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1778  
QY 1783 GGGGCGCTGCTGTGGCAAAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1842  
Db 1779 GGGGCGCTGCTGTGGCAAAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1838  
QY 1843 AGCCGAGTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1902  
Db 1839 AGCTTAAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1898  
QY 1903 GAGGATGTGCGAGCGTCTGTGCAATGCTGTGCTGACCCCTGTCTACAAAGTGTACG 1962  
Db 1899 GAGGCGTGTGCGAGTGTCTGTCTATAGTCTGCGCTGACCCCTGTCTACAAAGTGTACG 1958  
QY 1963 GCTGCTTTAAACATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2022  
Db 1959 GCTGCTTTAAACATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2018  
QY 2023 AGAATCAAACTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2082  
Db 2019 AGAATCAAACTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2078  
QY 2083 GATGCAATAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2142  
Db 2079 GATGCAATAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2138  
QY 2143 CAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2202

2139 CAAGCAGGAGAGCTGGCGGTTGGAGAGAAATACTTAAAGCTGGTCCATCGGGTTGCT 2198  
2203 GGTGTTGATTTATGCTCTAAATTTGATTTCTTGGAAACCAACTGATCAACAAATTTGGCAA 2262  
2199 GGTGTGATTTACGCTTTAAGTTGATCTTTGGAAACCAAGCTGAATCAAAACAACTGGCAA 2258  
2263 GAACTTCTTGCGCGCGCTTCTCTTATAGATAGACTGTTGTTGAAATTTCTCTGCTGAATTT 2322  
2259 GAACTGCTGGTGGCTCTGCTTATATAGACAGGTTGCTGTTGAAATTTCTCTGCTGAATTC 2318  
2223 TATCTCATATTTGTCAGTACTGATGTTTCAACAGCTGAGGCTGTTGAAATCAGGTATAG 2382  
2319 TATCTCATATTTGTCAGTACTGATGTTTCAACAGCTGAGGCTGTTGAAATCAGGTATAG 2378  
2383 AAGCTGCTGCTCTTAACTTTGCTTTGCTGAGTCCATTTGATTAATTTCCCACTCAATGTT 2442  
2379 AAGCTGCTCTCTCTTAACTTTGCTTTGCTGAGTCCATTTGATTAATTTCCCACTCAATGTT 2438  
2443 GGCMAAATTTCAGAGAGATCTACTGAGTTCTGCAAGATGTTTACTACAGTACCCCAT 2502  
2439 GGCAGGCTCTCTGGAGGATATATCTGAGCTCTGCCAGGATGTTGACCCAGTGGCGCT 2498  
2503 GTGTTTTCAAACTGTTAGAAATCTCTGAGTGTCTTCCAGTTTCCACTCACTCCAGGATG 2562  
2499 GTGTTTTCAAGCTGGTAACTGCTTAACTGCTTCTGCTCCACCTCACTCCAGGATG 2558  
2563 CGTCCGCGTTGATGCTATTTGAGATGAGTGGAAATTTGCGAGGCCATCCAGTTGGCG 2622  
2559 CGCGGCGCTCTGATGGCTATCGCGGATGAGTAGAAATTTCCGAGGTCATCCAGCTGGGT 2618  
2623 GTAGAAGACACTTTGGATGTTCAACAGAGACAGCTTCTTGAGGATCTGTTCCCAACAAC 2682  
2619 GTGAGGACACTGTGGATGGCATCAGGACAG----CTTACAGCGCTGGGCCCCCACCAGC 2675  
2683 TATCTGMAAACCAAGAGAACAGTTTCCCTGAGTGACAGTCCATTTAGAGAGAAAATCTGGA 2742  
2676 TGTCT-----AGAAAACAGCTCCCTTGAGCACACAGTCCATAGAGAGAAAATCTGGA 2726  
2743 AAAGGATTTATGCTTACAAAATTTGAGTCCAGTTTCAAGAGGACATTTCTGAGAGACTGGCC 2802  
2727 AAAGGACTTAACTGCTACAGACTGAGTGGCTGAGCTGGAGGACATTTCTGACAGACTGGCC 2786  
2803 AGCAATTCAGTAGGACCTTCTAGTTTCAACAAACAAACAAACAAACAAACAGAGCAACCA 2862  
2787 GSCGTCTCTGAGGACTTCCAGCT-----CAACAAACAAACAGAACCA 2831  
2863 AAGCAATGTTTCAAAACAAAGGAGAGACCCACAGTCACTGTTTGAATCTCTCCCTTA 2922  
2832 AAGCAGCGGTTTCAAAACAAAGGAGAGACCCACAGTCACTGTTTGAATCTCTCCCTTTG 2891  
2923 TCTCATCATTTCCAAATTAATGTTTCCAGCCTTGTCAACCCCTTCTTCTTACCCCATCT 2982  
2892 TC---TCATGCTCAATTAATGTTTCCAGCACCATCAGCCCTTGTTCCTCTGCCCCGTCT 2948  
2983 GTACAGCTGGGACTGCAACAGATGTTCTAAGCATAGACTTCAAGGATTCATTTCCCTGC 3042  
2949 GTCC-----CAGATTTCTAAGCACACAGCCCGGATTTGTTCCCTGCT 2993  
3043 AGAATACCTTCTGCACTCTCTCAAAACACAGGCGAGTTTCTCTACAAATTTCCACAGAAAC 3102  
2994 AAAATACCTTCCGATCTCTCAGACACAGCGCAAGTTCTCTCTACAAATTTCCAGAGAAC 3053  
3103 TGTCTGMAAACAAAGACTCAGATAAATTTCCCGAGTCTTACTCAGTCAAGACCTTG 3162  
3054 TGTCTGMAACACCGAGACTCAGACCAGTCTCTCCAGTCTTCACTCAGTCAAGACCCCCA 3113  
3163 CCTCCAGTAAACATACAGAGGCAAGGCACTAGACCTACCCAGGTAATACAAAGTAAA 3222  
3114 CCTCCAGTAAACATACAGAGGCAAGGCACTCCCGCGGTCGCGGCGAGTACAGCAA 3173  
3223 CAGGGAGATCCCTCAAAAATTAAGCATGACACTTGAATCTGMAAGTATCTCAATGTCAT 3282

3174 CTAGGGACGCCACAAAAGTAGCATGACACTTGAATCTGGCAGTGTCTCCAGGTGTGAC 3233  
3283 GACAGCTTTGGCTCTAGCAGCAATAGTAGTAATGCTGTATATCCCACTGACGAGACAGTG 3342  
3234 GACAGCTTTGGCGCGCGGCAACAGTGGCAACGCGCTCATATCCCAAGCAGACAGTGT 3293  
3343 TTCAACCCAGTAGAGAGAAATGACAGATTAGATTGATTAATACAGAGCTCAATCCAGTATT 3402  
3294 TTCAGCGCGTGGAGGCAAGTGCAGGTTAGATTGTAACCCGAGCTCAATCCAGGATC 3353  
3403 GAGGACCTTTCTGAAGCATCTATGCTTCAAGTATGATACAAACAGTAACTTTTAAGTCAGAA 3462  
3354 GAGGACCTTTCTGAAGCATCTATGCTTCAAGTATGATACAAACAGTAACTTTTAAGTCAGAA 3413  
3463 GTTGTGCTGCTCTCTGAAAAGGCTGAAATGATGATACCTTACAAAGATGATGTAAT 3522  
3414 GTGCGCGTCTCTCTCGGAAAAGCGGAAAATACGACACCTTACAAAGACAGCTCAAT 3473  
3523 CATTAATCAAAAGTTCGAAAGAGAGATGAAAGCTCAAGAAAGAAAGCTTTTAGCAATTTGCC 3582  
3474 CATTAATCAAAAGTTCGAAAGAGAGATGAAAGCTCAAGAAAGAGAGCTTTTAGCGATGCC 3533  
3583 ATGGCAATGTGAGCGTCTCAGGATGCGCTCCCATAGTTTCTCAGCTGAGGTTGAAAT 3642  
3534 ATGGCGATGTGAGCGTCTCAGGATGCGCTCCCATAGTTTCTCAGCTGAGGTTGAAAT 3593  
3643 GGAGAGATATCATCATTTTCAACAGGATACACAGAGACTCTACAGGACATACCAAA 3702  
3594 GGAGAGATATTTATCATCTTACGAGGACACACAGAACTCTTCCAGGACATACCAAA 3653  
3703 GCAAAACACCGTATAGAGAGACACATGATGGCTGAAAGTCAACAGATAGGCTTGGGA 3762  
3654 GCAAAACACCGTATAGAGAGAGACATGATGGCTGAAAGTCAACAGATAGGCTTGGGA 3713  
3763 GCAATTTCTCTGTTATCAGGCTCAAGATGTTGGAACTGGAATTTTAAATGGCTGTTAAA 3822  
3714 GCAATTTCTCTGTTATCAGGACAGGATGTTGGGACTGGGACTTTAATGGCTGTGAA 3773  
3823 CAGGTGACTTATGTGAGAAACACATCTTCTGAGGAAAGAAAGTAGTAGAGACTAAGA 3882  
3774 CAGGTGACTTATGTGAGAAACACATCTTCCGAGCAGGAGGAGTGTGGAAAGCTTGGG 3833  
3883 GAAGAGTAAAGTATGATGAGGATCTGAAATCATCAAAACATCATTTAGGATGTTGGGAGCC 3942  
3834 GAAGAGTCCGATGATGGTCACTCAACCATTCGAAACATCTCCGAGATGCTGGGGGCC 3893  
3943 AGGTGTGAGAGAGCAATTTACAATCTCTTCAATGATGATGGCAGGAGGATCGGTGGCT 4002  
3894 AGGTGTGAGAGAGCAATTTACAATCTCTTCAATGATGATGGCAGGAGGATCTGTGGCT 3953  
4003 CATTTGCTGATTAATGATGAGGCTTCAAGAACTAGTAGTTATTAATACACTGAAACAG 4062  
3954 CACCTTTGAGTAAATACGAGGCTTCAAGGAGTCACTCGTCAATTAATCACTGAGCAG 4013  
4063 TTACTCCGTGGCTTTCTGATCTCCATGAAAACCAAAATCTTCAAGAGATGTCAAAGT 4122  
4014 TTACTCCGTGGCTTTCTGATCTCCATGAAAACCAAAATCTTCAAGAGATGTCAAAGT 4073  
4123 GCCAATTTGCTAATGACAGGCTTCAAGAACTAGTAGTTATTAATGAGATGTTGGGCTGCA 4182  
4074 GCCAATTTGCTAATGACAGGCTTCAAGAACTAGTAGTTATTAATGAGATGTTGGGCTGCA 4133  
4183 GCCAGGTTGGCATCAAAAGGAACTGTTGAGGAGAGTTTCCAGGGAACAATTTACTGGGGACA 4242  
4134 GCCAGGTTGGCATCAAAAGGAACTGTTGAGGAGAGTTTCCAGGGAACAATTTACTGGGGACA 4193  
4243 ATTGCATTTATGGCACTGAGGATCTAAGAGTCAACAGTATGGAAGGAGCTGTGATGA 4302  
4194 ATTGCATTTATGGCACTGAGGATCTAAGAGTCAACAGTATGGAAGGAGCTGTGATGA 4253  
4303 TGAGGTTGGCTGTGCTTATTAAGAAATGGCTTGTGCAAAACCAACCTTGGAAATCAGAA 4362  
4254 TGAGGTTGGCTGTGCTTATTAAGAAATGGCTTGTGCAAAACCAACCTTGGAAATCAGAA 4313

QY 4363 AAACACTCAATCTCTTGGCTTTGATATTTAAGATTGCTAGTGCACCTACTGTCTCCATCG 4422  
 DB 4314 AAACACTCAATCTCTCTGCTTGAATTTAAGATTGCTAGTGCACCTACTGTACCGTCC 4373  
 QY 4423 ATCCCTTACATTTGCTCTCTGCTTTACGAGATGCTCTCTCTTTAGAACTTCAA 4482  
 DB 4374 ATCCCGTACACCTGTCTCCCGCTCTGCGCAGCTGCGCTGCTTTAGAACTTCAG 4433  
 QY 4483 CCTCAGGACAGCTCCATCAAGAGAGCTACTGAAGCATCCAGTCTTTCTGCTACTACATGG 4542  
 DB 4434 CCTCAGGACCGCTCTCTGCTCAGAGAGCTGCTGAACATCCGCTCTTCCGTACCACTGG 4493  
 QY 4543 TAGCCAAATATGAGATCAATACAGTAGAAGAGAGTGTCTCAACAGAGAGAGAGAACT 4602  
 DB 4494 TAGTTAATTTGCTAGATCAGCTCTAATGAGACAGAGATATGCAACCGGAGAGAGAAAG 4553  
 QY 4603 TG---TGGGGAACACATTTGATATCTTACTGGCCATGATGCCACTGAACAGCTATGAAC 4658  
 DB 4554 AGAACTTGTGGGACCAATGCGCTAACCGCAGCCCTCAGCCACTGAACAGCCAGAAC 4613  
 QY 4659 GAGGCCAGTGGGGAACCTTACCTAAGTATGTGATTGACAAATCATGATCTGTACCTAAG 4718  
 DB 4614 GGGGCCAGCGGGAA-CGGTACCTAAGCATGTGATTGACAAATCATGACCTGTACCTAAG 4672  
 QY 4719 CTCAGTATGCA-AAAGCCCAACTAGTGCAGAACTGTAACTGTGCTTTCAAGAACT 4777  
 DB 4673 CTCGATATGCAAGATCTTACAGCTCGTGCAGAACTGCACACCGTGTCTTTACAGGACT 4732  
 QY 4778 GGCCTTAGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4837  
 DB 4733 GGCTCTGGGGACAGGAGCGGATGGAGTTTGCATGACTTAAAGAACAGAGAGAGAGAG 4792  
 QY 4838 TATTTTTTGGAGCACTTTTTCAGCAA 4864  
 DB 4793 TA--TTTGGAGCACTTTTTCAGCTA 4817

## RESULT 12

AD44414  
 ID AD44414 standard; DNA; 5253 BP.

AC AD44414;

DT 13-DEC-2002 (first entry)

DE Mouse MEK1 DNA.

XX Mitogen-activated protein kinase; MAPK; MAPK kinase; MEK; MEK kinase 1;  
 KW MEK1; apoptosis; caspase protease; anti-apoptotic; autoimmune disease;  
 KW allergic reaction; inflammation; neurological disorder; cancer;  
 KW hormone-related disease; apoptotic; cytostatic; immunosuppressive;  
 KW antiinflammatory; nootropic; neuroprotective; endocrine-gen; mouse;  
 KW enzyme; gene; ds.

XX Mus musculus.

XX Key Location/Qualifiers

FT CDS 15..4496

FT /tag= a

FT /product= "Mouse MEK1"

PN US2002055130-A1.

XX 09-MAY-2002.

XX 16-MAY-2001; 2001US-00858754.

XX 14-FEB-1997; 97US-0039740P.

XX 13-FEB-1998; 98US-00023130.

XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

XX

PI Johnson GL;

XX WPI: 2002-462905/49.

DR P-PSDB; AAE26657.

XX New isolated protease resistant mitogen-activated protein kinase kinase  
 PT kinase protein used for inhibiting apoptosis and treating diseases, such  
 PT as, cancer, autoimmune diseases, allergic reactions, and inflammation.

XX Disclousure; Page 68-73; 97pp; English.

XX The invention relates to protease-resistant mitogen-activated protein  
 CC kinase (MAPK) kinase (MEK) kinase 1 protein, designated MEK1 and its  
 CC corresponding nucleic acid. MEK1 is used to inhibit apoptosis. MEK1  
 CC fragment is used to stimulate apoptosis. The fragment is used to identify  
 CC a compound that modulates the apoptotic activity of the fragment. MEK1  
 CC is used to identify a compound that modulates the proteolytic cleavage of  
 CC the protein by a caspase protease is used to treat diseases such as  
 CC cancer, autoimmune diseases, allergic reactions, inflammation,  
 CC neurological disorders, or hormone-related diseases. The present sequence  
 CC is mouse MEK1 DNA

XX Sequence 5253 BP; 1299 A; 1403 C; 1433 G; 1118 T; 0 U; 0 Other;

XX Query Match 65.1%; Score 3417; DB 6; Length 5253;

XX Best Local Similarity 83.5%; Pred. No. 0;

XX Matches 4081; Conservative 0; Mismatches 705; Indels 101; Gaps 14;

QY 1 GAGAAATGCGCGCGCGCGCGGGAATCGCGCTCTGCTCGTCCGGATTCCCGGCGCCAGG 60

DB 9 GAGAAATGCGCGCGCGCGCGCGGCGATCGCGCTCTGCTCGGATTCCCGGCGCCAGG 68

QY 61 GCTACGAGCCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 111

DB 69 GCGCGAGTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 128

QY 112 GCGCCC---GCGCGTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 168

DB 129 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 188

QY 169 GCGGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 228

DB 189 GCGGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 248

QY 229 GAGCAGCGCGCTCTCTCTTCCCGCGCTCACCGCGCGCGCT---CCTCGACTTCCCGTCCGCG 285

DB 249 GAGCAGCGCGCTCTCTCTTCCCGCGCGCTCACCGCGCGCGCTTCTTCCCGTCCGCGCG 308

QY 286 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 345

DB 309 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 368

QY 346 CACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 405

DB 369 CCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 428

QY 406 GCGCGCTCGAGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 465

DB 429 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 458

QY 466 TCTCTTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 525

DB 459 CCTCTTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 518

QY 526 CACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 585

DB 519 CACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 578

QY 586 ATGCCAGCTTGAAGCAGCAAGATGTTGAAAGAGAGAAATAGCGAGCGCGCTGTGTGTGTA 645

DB 579 ATGCCAGCTTGAAGCAGCAAGATGTTGAAAGAGAGAAATAGCGAGCGCGCTGTGTGTGTA 638

QY 646 AAACCAATCCAGTTAAAGAGATGATCTGAATGAATCACTTAGCAGCTGAGTCTCCA 705

|    |      |                                                                 |      |      |                                                               |      |
|----|------|-----------------------------------------------------------------|------|------|---------------------------------------------------------------|------|
| Db | 639  | AAGCCAAATCCCTATTTAAAGGAGATGSGATCTGAAGTGAATACCTTGGCAGCTGAGCCCCAG | 638  | 1719 | TTCTCTAGAAACTGGAACTGAAGGAAATGSCCTTAGGCGTCTTTCCACGACGTTAGT     | 1778 |
| Qy | 706  | GGAGAGGTCAGGCAAGTGCAGCTTACACAGCTTCCAAAGCCGACAGCAGTCTCTCTCT      | 765  | 1783 | GGGGCCCTGCTGTTGGGAAATGGGAGAGCACTGGAAATTTCTGGGGGAGCAGTGGGAGC   | 1842 |
| Db | 699  | GGAGAGGTCAGGCAAGTGCAGCTTACACAGCTTCCAAAGCCGACAGCAGTCTCTCTCT      | 758  | 1779 | GGGGCCCTGCTGTTGGGAAATGGGAGAGCACTGGAAATTTCTGGGGGAGCAGTGGGAGC   | 1838 |
| Qy | 766  | GGCACTCCCATCAGGTCGACAGTGAATCAGAACTCAGAGTAAGGAGAGAAAGA           | 825  | 1843 | AGCCCGAGTGGGGAGCCACCAAGTGGGTCTTCCAGAGCCAGTATCTCAGAGAGATGTGGTG | 1902 |
| Db | 759  | GGCAGCTCTCCGTCAGGCGCTCGGTGAAGCGGAAATCCCGAGAGTAAGACGGAACGA       | 818  | 1839 | AGCTTAAGCGCGGAGCGCCAGCGGTCTCCAGCCAGCACTCTCAGGGAGATGTGGTG      | 1898 |
| Qy | 826  | GTITCCCGAGTGCCTTTTACAGTGGGAGAGTACACACACCCCGAGAGCCCTTACCCA       | 885  | 1903 | GAGGCACTGTCAGCGTTCTGTCAATGTCTGTCTGCTGACCTGTCTACAAAGTGTACCTT   | 1962 |
| Db | 819  | GTGTCCCGGTGCCTTTTCCAGTGGGAGAGTACACACACCCCGAGAGCCCTTACCCA        | 878  | 1899 | GAGGCGTGTGTCAGTGTCTGTCTATAGTCTGCGCTGACCTGTCTACAAAGTGTACCTT    | 1958 |
| Qy | 886  | GATGCTTCTCACATATAGCCCTGAGGAAACAAACCGCGGTGTTTACAAAGTGTACCGG      | 945  | 1963 | GCTGCTTTTAAAAACATTCAGAGCCATGCTGTATATCTCTCTTGGCCACAGTTTACGGAA  | 2022 |
| Db | 879  | GATGCTTCTCACATATAGCCCTGAGGAAACAAACCGCGGTGTTTACAAAGTGTACCGG      | 938  | 1959 | GCTGCTTTTAAAAACATTCAGAGCCATGCTGTATATCTCTCTTGGCCACAGTTTACGGAA  | 2018 |
| Qy | 946  | GCCAGCTGTACTTACTGCAGCAGATAGGGCTTAACCTTTCTCTGATTGGAGGAGACAGC     | 1005 | 2023 | AGAAATCAAACTTCAGAGACTTCTCAGCCAGTTGTAGACACCATCTCTAGTCAAAATGTCA | 2082 |
| Db | 939  | GCCAGCTGTACTTACTGCAGCAGATAGGGCTTAACCTTTCTCTGATTGGAGGAGACAGC     | 998  | 2019 | AGAAATCAAACTTCAGAGACTTCTCAGCCAGTTGTAGACACCATCTCTAGTCAAAATGTCA | 2078 |
| Qy | 1006 | CCAGCAATAAATACCGGGTGTATTGGGCTCAGAACTCAGACTGTCAGCTGTGGAACA       | 1065 | 2083 | GATGCCAATAGCCGACCAAGTCAGCTGTCCATATCAACACTGTTGAAACTGTGCAAAAGC  | 2142 |
| Db | 999  | CCAGCAATAAATACCGGGTGTATTGGGCTCAGAACTCAGACTGTCAGCTGTGGAACA       | 1058 | 2079 | GATGCCAATAGCCGACCAAGTCAGCTGTCCATATCAACACTGTTGAAACTGTGCAAAAGC  | 2138 |
| Qy | 1066 | TTCTGTATTCATCTGCTATTTGTGATGCTCCGGGTGTTTCAACTAGAACCTTTCAGACCA    | 1125 | 2143 | CAAGCAGGAGAGTTGGCAGTTGGCAGAGAAATATCTAAAGCTGGATTCATTTGGT       | 2202 |
| Db | 1059 | TTCTGTATTCATCTGCTATTTGTGATGCTCCGGGTGTTTCAACTAGAACCTTTCAGACCA    | 1118 | 2139 | CAAGCAGGAGAGTTGGCAGTTGGCAGAGAAATATCTAAAGCTGGATTCATTTGGT       | 2198 |
| Qy | 1126 | ATGTTATGAGGAAACCTTTAAAGAAATTTGAGGTTGAGGTTGTTTCCAGAAATATCAC      | 1185 | 2203 | GGTGTGATTGTTGCTTAAATGTTATCTTGGAAACCAAACTGAAATCAAACTTGGCAA     | 2262 |
| Db | 1119 | ATGTTATGAGGAAACCTTTAAAGAAATTTGAGGTTGAGGTTGTTTCCAGAAATATCAC      | 1178 | 2199 | GGTGTGATTGTTGCTTAAATGTTATCTTGGAAACCAAACTGAAATCAAACTTGGCAA     | 2258 |
| Qy | 1186 | AGTAGGCTGAGCTCAGAGTCAAGCTCCATCTGTAACACCACTCCAGAGTTTGTTC         | 1245 | 2263 | GAACTCTTGGCGCCTTTGCTTATAGATAGACTGTTGTTGAAATTTCTCTGCTGAATTT    | 2322 |
| Db | 1179 | AGTAGGCTGAGCTCAGAGTCAAGCTCCATCTGTAACACCACTCCAGAGTTTGTTC         | 1238 | 2259 | GAACTCTTGGCGCCTTTGCTTATAGATAGACTGTTGTTGAAATTTCTCTGCTGAATTT    | 2318 |
| Qy | 1246 | CGCATGTCAATTTCTACATATGTCATCTAGTACTTCTAGCTGTAGTTCAGAAAC          | 1305 | 2323 | TATCTCTATTTTCAGAGGATCTACTTGTGCTTCTGCAAGATGTTTGAATCAGGTATTAAG  | 2382 |
| Db | 1239 | CGCATGTCAATTTCTACATATGTCATCTAGTACTTCTAGCTGTAGTTCAGAAAC          | 1298 | 2319 | TATCTCTATTTTCAGAGGATCTACTTGTGCTTCTGCAAGATGTTTGAATCAGGTATTAAG  | 2378 |
| Qy | 1306 | AGCATTAAGGATGAGAGGACAGATGTCTTATTTCTGTTGGGATGCTTGTATGA           | 1365 | 2383 | AAGCTGCTGCTCCCTTTAACTTTGCTTTCAGAGTCCATTTGAATTTCCCACTCAATGGTT  | 2442 |
| Db | 1299 | AGCATTAAGGATGAGAGGACAGATGTCTTATTTCTGTTGGGATGCTTGTATGA           | 1358 | 2379 | AAGCTGCTGCTCCCTTTAACTTTGCTTTCAGAGTCCATTTGAATTTCCCACTCAATGGTT  | 2438 |
| Qy | 1366 | GAAAGTCTTACAGTGTGAGAGCGCTGCGAGAAACAGCTGCACCACTGCATGTCA          | 1425 | 2443 | GGCAAACTTTCAGAGGATCTACTTGTGCTTCTGCAAGATGTTTGAATCAGGTATTAAG    | 2502 |
| Db | 1359 | GAAAGTCTTACAGTGTGAGAGCGCTGCGAGAAACAGCTGCACCACTGCATGTCA          | 1418 | 2439 | GGCAAACTTTCAGAGGATCTACTTGTGCTTCTGCAAGATGTTTGAATCAGGTATTAAG    | 2498 |
| Qy | 1426 | ATTTGGGAGAGAGTGTAGAGAAATAGAGAACCTTTTATATGTCCTCTTGTAGATCT        | 1485 | 2503 | GTGTTTTCAAACTGTTAGAAATGCTGAGTGTTCAGTTCACCTCACTTCCAGGATG       | 2562 |
| Db | 1419 | ATTTGGGAGAGAGTGTAGAGAAATAGAGAACCTTTTATATGTCCTCTTGTAGATCT        | 1478 | 2499 | GTGTTTTCAAACTGTTAGAAATGCTGAGTGTTCAGTTCACCTCACTTCCAGGATG       | 2558 |
| Qy | 1486 | AAGTGAGATCTCATGATTTCTACAGCCACAGTGTCTCAAGTCTCTGTGATTTCCCTTCT     | 1545 | 2563 | CGTGGCGCTTGTAGTGTATTCAGATGAGGTGGAATTTCCAGAGCCATCCAGTTGGGC     | 2622 |
| Db | 1479 | AAGTGAGATCTCATGATTTCTACAGCCACAGTGTCTCAAGTCTCTGTGATTTCCCTTCT     | 1538 | 2559 | CGCAGCGCTGTGATGCTTTCGCGATGAGGTAGAAATTTCCAGAGTTCATCCAGCTGGGT   | 2618 |
| Qy | 1546 | TCCTCAGAGTGCACAGAGCAACCGGTACAGAGCAGCCTTTGGCTGGATCA---CGA        | 1602 | 2623 | GTAGAGACACTTTGATGCTTCAACAGGACAGCTTCTTTCAGGACATCTGTTCACCAACAC  | 2682 |
| Db | 1539 | TCCTCAGAGTGCACAGAGCAACCGGTACAGAGCAGCCTTTGGCTGGATCA---CGA        | 1598 | 2619 | GTAGAGACACTTTGATGCTTCAACAGGACAGCTTCTTTCAGGACATCTGTTCACCAACAC  | 2675 |
| Qy | 1603 | AGGAATCAAGAGAGCAATTTTAACTTACTTATGGAATCTCAGCAAAATCCCTCTGCT       | 1662 | 2683 | TATCTGGAACACACAGAGAACAGTTCCTCTGAGTGCACAGTCCATTTAGAGAACTGGA    | 2742 |
| Db | 1599 | AGGAATCAAGAGAGCAATTTTAACTTACTTATGGAATCTCAGCAAAATCCCTCTGCT       | 1658 | 2676 | TGTCT-----AGAAACAGCTCCCTTTGAGCACACAGTCCATAGAGAGAACTGGA        | 2726 |
| Qy | 1663 | TACAAAGATTTAGCTCAGCACTGATTCAGGTGTTTGGATGGAACTGCTGGCTGCTTA       | 1722 | 2743 | AAAGGATTTATGCTTACAAATTTAGTTCAGTTCAGAGGACATTTCTGAGAGACTGGCC    | 2802 |
| Db | 1659 | TACAAAGATTTAGCTCAGCACTGATTCAGGTGTTTGGATGGAACTGCTGGCTGCTTA       | 1718 | 2727 | AAAGGATTTATGCTTACAAATTTAGTTCAGTTCAGAGGACATTTCTGAGAGACTGGCC    | 2786 |
| Qy | 1723 | TTTTCTAGAACTGGAAATGAGAGAGATGGCCTTCAGGCTCTTTTCCCATGATGTCA        | 1782 | 2803 | AGCATTTTCAAGACCTTCTAGTTCACAAACAAACAAACAAACAAACAAACAAACAAAC    | 2862 |
|    |      |                                                                 |      | 2787 | GGCGTCTCTAGAGACTTCCAGCT-----CAACAAACAAACAAACAAACAAAC          | 2831 |

QY 2863 AAGCAATGGTTCAAAACAAAGGAGAGACCCACAGTCAGTGTGTTGAACTCCTCTCCCTTTA 2922  
DB 2832 AAGCAGCGGTTCAAAACAAAGGAGAGACCCACAGTCAGTGTGTTGAACTCCTCCCTTTG 2891  
QY 2923 TCTCATCTCCCAATTAATGTTTCCAGCCTGTCAAACCCCTTCTTCTTCTTACCCCATCT 2982  
DB 2892 TC---TCATGCTCAATTAATGTTTCCAGCAGCACCATCAGCCCTTGTCTCTGCCCCGCT 2948  
QY 2983 GTACAGCTGGCACTGCAACAGATGTCTTAAGCATAGACTTTCAGGATTCATTCCTGSC 3042  
DB 2949 GTCC-----CAGATATTCAGCAGACCCAGGCAATTTGTTCCCTGSC 2993  
QY 3043 AGAATACCTTCTGATCTCTCTCAACACAGCCCAAGTCTTCTTCAATTCACAGAAAC 3102  
DB 2994 AAAATACCTTCCGCACTCTCTCAGACACAGCCCAAGTCTTCTTCAATTCAGAGAAC 3053  
QY 3103 TGTCTCTGAAAACAAAGACTCAGATAAATTTCCCCAGTCTTCTTACTCAGTCAAGACCTTTG 3162  
DB 3054 TGCTCTGACACCGAGACTCAGACAGCTCTCCAGTCTTCTTCACTCAGTCAAGACCCCA 3113  
QY 3163 CCTTCCAGTAACATACACAGGCAAGGCACTTACAGCTTACCCAGGTAATACAGATAA 3222  
DB 3114 CCTTCCAGTAACATACACAGGCAAGGCACTTCCAGCCGTTCCGCGCAGTACAGACAA 3173  
QY 3223 CAGGAGATCCCTCAAAAATAGCATGACACTTGTATGAAACAGTAGTTTCCAAATGTGAT 3282  
DB 3174 CTAGGGAGCCCAAAAAGTAGCATGACACTTGTATGATCTGGGAGTGTCTTCCAGTGTGAC 3233  
QY 3283 GACAGCTTTGGTGTAGAGCAATAGTAGTAATGTGTTTATACCCAGTGAACAGACAGTG 3342  
DB 3234 GACAGCTTTGGCGCGCGGCAACAGTGGCAACCGCGCTCATACCCAGCGACGAGACAGTG 3293  
QY 3343 TTCACCCAGTAGAGAGAAATGCAATAGATGTCAATACAGAGCTCAACTCCAGTATT 3402  
DB 3294 TTCCGCGGTGAGGACAAAGTGCAGTTAGATGTGAACACCGAGCTCACTTCCAGCATC 3353  
QY 3403 GAGGACCTTCTTGAAGCATCTATGCTTCAAGTGATACAAACAGTAACCTTTAAGTCAGAA 3462  
DB 3354 GAGGACCTTCTTGAAGCATCTATGCTTCAAGTGATACAAACAGTCACTTTCAAGTCGAA 3413  
QY 3463 GTTCTGCTCTGCTCTGTAAGAGGCTGAATATGATGTATCTTACAAAGATGATGTGAAT 3522  
DB 3414 GTCCGCTCTCTCTCCGGAAGAGGCGAAATGACGACCTTACAAAGACGAGTCAAT 3473  
QY 3523 CATAATCAAAAGTCAAGAGAGATGGAAGCTGAAGAGAGAAAGCTTTAGCAATTTGCC 3582  
DB 3474 CATATCAAAAGTCAAGAGAAAGATGGAAGCTGAAGAGAGAGGCTTTAGCGATCGCC 3533  
QY 3583 ATGGCAATGTCAGGCTCAGGATGCGCTCCCATAGTTCCTCAGCTGCAAGTTGAAT 3642  
DB 3534 ATGGCGATGTGAGGCTCAGGATGCGCTCCCATGCTCCCTCAGCTGCAAGTGAAT 3593  
QY 3643 GGAGAGATATCATATTATCAACAGGATACACAGAGACTCTACAGGACATACCAA 3702  
DB 3594 GGAGAGATATATCATATTACAGGACACACAGAGAACTCTTCCAGGACATACCAA 3653  
QY 3703 GCAAAACACCGTATAGAGAGACACATGAATGCTGAAGGTCAACAGATAGGCTTGA 3762  
DB 3654 GCGAAACAGGCTTACAGAGAGACGCTGAGTGTGCTGAAAGGCCAGCAGATAGGCTTCGA 3713  
QY 3763 GCATTTCTTCTTGTATCAGGCTCAAGATGTGGGAACCTGGAATTTAATGGCTGTAAA 3822  
DB 3714 GCATTTCTTCTTGTATCAGGACACAGGATGTGGGACTGGGACTTTAATGCTGTGAA 3773  
QY 3823 CAGTGACTTATGTGAGAAACACATCTTCTTGAGCAAGAGAAAGTAGTAGAGCACTAAGA 3882  
DB 3774 CAGTGACGTACGTGAGAAACACATCTCCAGCAGGAGGAGTGTGGAAGGCTTGAAG 3833  
QY 3883 GAGAGATAGATGATGAGCCATCTCAATCATCCCAACATCATATTAGGATGTTGGAGCC 3942  
DB 3834 GAGAGATCCGATGATGGGTACCTTCAACCATCCAAACATCATCCGATGCTGGGGCC 3893

QY 3943 ACCTGTGAGAGAGCAATTAACAATCTCTTCAATTGAATGATGCGAGGGGATCGGTGGCT 4002  
DB 3894 ACCTGTGAGAGAGCAATTAACAATCTCTTCAATTGAATGATGCGAGGGGATCGGTGGCT 3953  
QY 4003 CATTTGCTGAGTAAATATAGGAGCTTTCAAAGATCAGTAGTATTATTAACTACACTGAACAG 4062  
DB 3954 CACTCTTGAATAAATACGAGGCTTTCAAGGAGTCACTGCTCATTAACACTGAGCAG 4013  
QY 4063 TTACTCCGCTGGCTTCTGCTATCTCCATGAAGAACCAAAATCAATTCACAGAGATGCAAGGT 4122  
DB 4014 TTACTGCTGGCTTCTCTATCTCCAGAGAACAGATCATTCACAGAGACGTCGAAGGT 4073  
QY 4123 GCCAATTTGCTAATTCAGACACTGTTCAGAGACTAAGAAATTCAGATTTTGGAGCTGCA 4182  
DB 4074 GCCAATCTGCTCAATTCAGACACCGGTTCAGAGCTGAGATTCAGACTTTGGAGCTGCT 4133  
QY 4183 GCCAGGTTGGCATCAAAGGAACTGTGTGAGAGAGATTTTCAGGCAAAATTAATCTGGGACA 4242  
DB 4134 GCCAGGTTGGCATCAAAGGAACTGTGTGAGAGAGATTTTCAGGCAAAATTAATCTGGGACA 4193  
QY 4243 ATTGCATTTATGCACTGAGTACTAAGAGGTCAACAGTATGGAAGGAGCTGTGATGTA 4302  
DB 4194 ATTGCATTTATGCGGCTGAGGCTTAAAGAGGTTCAGAGCTGATGTAAGGAGCTGTGATGTA 4253  
QY 4303 TGGAGTGTGGCTGTGCTATTATAGAAATGGCTTTGTGCAAAAACCAATGGAATGCAAGAA 4362  
DB 4254 TGGAGTGTGGCTGTGGCTATTATAGAAATGGCTTTGTGCAAAAACCAATGGAATGCAAGAA 4313  
QY 4363 AAACACTCCCAATCATCTTGTGATATTAAGATGCTAGTCAACTACTGCTCCATCG 4422  
DB 4314 AAACACTCCCAATCATCTTGTGATATTAAGATGCTAGTCAACTACTGCTCCATCG 4373  
QY 4423 ATCCCTTCAATTTGCTCTCTGCTTTACGAGATGTGCTCTTCTGTTGTTTGAACCTTCAA 4482  
DB 4374 ATCCCTGTCACACCTGTCTCCCGGCTGTCGCGACGTCGCGCTGCTTTAGAACTTCAG 4433  
QY 4483 CCTCAGACAGACCTCCATCAAGAGACTACTGAGCATCCAGTCTTTCTGCTACTACATGG 4542  
DB 4434 CCTCAGACAGCGGCTCCGTCAGAGAGCTGCTGAACATCCGGTCTTCCGCTACCACTGG 4493  
QY 4543 TAGCCAATTTAGCAGATCAACTACAGTAGAAACAGGATGCTCAACAGAGAGAAACAACT 4602  
DB 4494 TAGTTAATTTGCTCAGATCAGCTCTAATGGAGACAGGATATGCAACCGGAGAGAGAAAG 4553  
QY 4603 TG---TGGGAAACCAATTGATATTCTTCTGCTCATGATGCCACTGCACTGAAACAGCTATGAAC 4658  
DB 4554 AGAACTTTGTGGCGACCATGCGCTAAACCGCAGCCCTCACGCCACTGAAACAGCGCAAAAC 4613  
QY 4659 GAGGCCAGTGGGAAACCTTTACCTTAAGTATGTGATTCACAAATCATGATCTGTACCTTAAG 4718  
DB 4614 GGGGCCAGCGGGAA-CCGTACCTAAGCATGTGATTCACAAATCATGATCCCTGTACCTAAG 4672  
QY 4719 CTCAGTATGCA-AAAGCCCAAACTAGTGCAGAAACTGTAAACTGTGCTTTCAGAGAACT 4777  
DB 4673 CTCGATATGCAAGACATCTACAGCTCGTGCAGAACTGCAACCGTGTCTTTCAGAGACT 4732  
QY 4778 GGCCCTAGTGAACAGGAAACCAATGAATTTGATGATCACTAAATTTGAGAGAGCAATATTT 4837  
DB 4733 GGCTCTGGGGACCCAGGAGGCGATGAGTTTGCATGATCTTAAGAAACAGAGCATATTT 4792  
QY 4838 TATTTTGTGAGCACTTTTTCAGCAA 4864  
DB 4793 TA--TTTTTGGAGCACTTTTTCAGCTA 4817

## RESULT 13

AAL41578 standard; cDNA; 5539 BP.

ID AAL41578

XX AAL41578;

AC AC

XX 19-APR-2002 (first entry)

DT

XX





Db 1846 AGACCTGACTGTGTGAAGATGGCTGCAAGAAACAGCTGCACCACTTGCATGTCCA 1705  
Qy 1427 TTTGGCAGAGAGTGTAGAAGAAATAGAGAACCTTTAATATGTATGTCCTTTGTAGATCTA 1486  
Db 1706 TCTGGCGGAAGAGTGTAGAAGAAATAGAGAGCCTTTAATATGTATGTCCTTTGTAGATCTA 1765  
Qy 1487 AGTGGAGATCTCATGATTTCTACAGCCACAGTGTCTCAAGTCTGTGGATCCCTCTCTT 1546  
Db 1766 AGTGGAGATCCCATGACTTCTACAGCCATGAGTGTATCAAGCCCGTGGATCCCGCCCT 1825  
Qy 1547 CCCTCAGAGTGCACAGCAGCAACCGTACAGCAGCAGCCTTTGGCTGGATCA ---CGAA 1603  
Db 1826 CCCTCGAGCTGTCCAGCAGCCTCTCCCGCAGCAGCCGCTGGCCGATCACAGCGGA 1885  
Qy 1604 GGAATCAAGAGAGCAATTTTAACTTACTCATATGAACTCAGCAAACTCCCTCTGCTT 1663  
Db 1886 GGAATCAGGAGAGAGTGTAACTTACTCATATTTGAAACCCAGCAGATTTCTTCGCTT 1945  
Qy 1664 ACAAAGATTTAGCTGAGCCATGGATTCAGGTGTGTGAATGGAACTGGTGGCTGCTTAT 1723  
Db 1946 ACAAGATTTGGCCGAGCATTGGATTCAGGTGTGTGAATGGAACTGGTGGCTGCTTAT 2005  
Qy 1724 TTTCTAGAACTGGAATGTAGAGAGATGGCCCTCAGGCGTCTTCCCATGATGTCAATG 1783  
Db 2006 TCTCTAGAACTGGAACGTAAAGGAAATGGCCCTTAGGCGTCTTCCCAACGATTTAGTG 2065  
Qy 1784 GGGCCCTCTGTGGCAATGGGAGAGCACTGGAATTTCTGGGGCAGCAGTGGAGCA 1843  
Db 2066 GGGCCCTGTGTGGCAACGGGAGAGCACTGGAATTTCTGGAGCGGCGAGTGGGGCA 2125  
Qy 1844 GCGGAGTGGGGAGCCACAGTGGGTCTCCAGACAGATCTCAGAGATGTGTGTG 1903  
Db 2126 GCTTAAGCGGGAGCGCCAGCGGTCTCCAGCCAGCATCTCAGGGGATGTGTGTG 2185  
Qy 1904 AGGATGCTGAGAGTCTGTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1963  
Db 2186 AGGCGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2245  
Qy 1964 CTGCTTTAAACATTTAGAGCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2023  
Db 2246 CTGCTTTAAACATTTAGAGCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2305  
Qy 2024 GAATCAAACTTCAGAGCTTCCAGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2083  
Db 2306 GAATCAAACTTCAGAGCTTCCCGCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2365  
Qy 2084 ATGCCAATAGCCGACAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2143  
Db 2366 ATGCCAATAGCCGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2425  
Qy 2144 AAGCAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2203  
Db 2426 AAGCAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2485  
Qy 2204 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2263  
Db 2486 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2545  
Qy 2264 AACTTCTGGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2323  
Db 2546 AACTTCTGGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2605  
Qy 2324 ATCCCTCATATTCAGTACTGATTTTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTG 2383  
Db 2606 ATCCCTCATATTCAGTACTGATTTTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTG 2665  
Qy 2384 AGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2443  
Db 2666 AGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2725  
Qy 2444 GCAAACTTCCAGAGGATCTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2503

Db 2726 GCAGCTCTCTCGGAGGATATATCTGAGCTCTGCCAGGATGGTGACCGAGTGCCTCGCTG 2785  
Qy 2504 TGTTTTCAAACCTGTGTAGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2563  
Db 2786 TGTTTTCAAAGCTGTGTAAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2845  
Qy 2564 GTCCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2623  
Db 2846 GCCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2905  
Qy 2624 TAGAAGACACTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2683  
Db 2906 TGGAGGACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2962  
Qy 2684 ATCTGGAACCAACAGAGAACAGTTCCTCTGTGTGTGTGTGTGTGTGTGTGTGTG 2743  
Db 2963 GTCT-----AGAAACAGCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTG 3013  
Qy 2744 AAGGATTTAGTGTCTCAAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2803  
Db 3014 AAGGACTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3073  
Qy 2804 GCATTTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2863  
Db 3074 GGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3118  
Qy 2864 AGCCAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2923  
Db 3119 AGCCAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3178  
Qy 2924 CTCTCATCTTCCAAATTAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2983  
Db 3179 C---TCATGTCTCAATTAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3235  
Qy 2984 TACCAGCTGGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3043  
Db 3236 TCC-----CAGATAATTTCTAAGCAGAGCAGCCAGGCAATTTGTTCCTGTGA 3280  
Qy 3044 GAATACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3103  
Db 3281 AAATACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3340  
Qy 3104 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3163  
Db 3341 GCTCTGAACAGCAGACTCAGACAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTG 3400  
Qy 3164 CTTCTAGTAACTATACAGGCGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3223  
Db 3401 CTTCTAGTAACTATACAGGCGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3460  
Qy 3224 AGGAGATCCCTCAAAATAGCATGACACTTGTGTGTGTGTGTGTGTGTGTGTGTG 3283  
Db 3461 TAGGGAGCGCCAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3520  
Qy 3284 ACAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3343  
Db 3521 ACAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3580  
Qy 3344 TCACCCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3403  
Db 3581 TCAGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3640  
Qy 3404 AGGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3463  
Db 3641 AGGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3700  
Qy 3464 TTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3523  
Db 3701 TCAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3760  
Qy 3524 ATAATCAAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3583  
Db 3761 ATAATCAAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3820



CC apoptosis can be produced. MEK1 proteins and antibodies immunoreactive  
CC with MEK1 proteins are used in diagnostic and therapeutic assays and  
CC reagents for detecting and treating disorders involving aberrant  
CC expression or activation of the MEK1 gene products. DNA probes or  
CC primers that selectively hybridise to MEK1 cDNA, can be used for its  
CC detection in samples  
XX  
SQ

Sequence 3911 BP; 1058 A; 973 C; 975 G; 905 T; 0 U; 0 Other;

Query Match 62.7%; Score 3286.4; DB 2; Length 3911;

Best Local Similarity 90.5%; Pred. No. 0;

Matches 3580; Conservative 0; Mismatches 331; Indels 45; Gaps 5;

590 CAGCCTCGAGGACGAGTGTGGAAGGAGAAATAGCGAGGCGCTGTGGTGGTAAAC 649

1 CGGCTCGAAGCAGCAGTGGTTGGAAGGAGAAATAGCGAGGCGCTGTGGTGGTAAAC 60

650 CAATCCAGGTAAAGGAGATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCCAGGAG 709

61 CAATCCAGGTAAAGGAGATGGATCTGAAATGAATCACTTAGCAGCTGAGTCTCCAGGAG 120

710 AGGTCGAGGAGTGGCGCTTCACGAGTTCAGAGGCGGAGGCTTCCTGGCA 769

121 AGGTCGAGGAGTGGCGCTTCACGAGTTCAGAGGCGGAGGCTTCCTGGCA 180

770 ACTCCCATCAGGTCGACAGTGAATCAGAACTCTCCAGGAGTAAGAGAGAAAGAGTTT 829

181 ACTCCCATCAGGTCGACAGTGAATCAGAACTCTCCAGGAGTAAGAGAGAAAGAGTTT 240

830 CCCAGTGCCCTTTCAGAGTGGAGAAATCACACCCCGAGAGGCCCTTCCAGGATG 889

241 CCCAGTGCCCTTTCAGAGTGGAGAAATCACACCCCGAGAGGCCCTTCCAGGATG 300

890 GCTTCTCACATATAGCCCTCAGGAAACAAACCCCGCTGTAAACAAAGTATGCGGCCCA 949

301 GCTTCTCACATATAGCCCTCAGGAAACAAACCCCGCTGTAAACAAAGTATGCGGCCCA 360

950 GACTGTACTACTGAGCAGATAGGCGCTAACTCTTCTGATGAGAGGAGAGAGCCAG 1009

361 GACTGTACTACTGAGCAGATAGGCGCTAACTCTTCTGATGAGAGGAGAGAGCCAG 420

1010 ACAATAAATACCGGCTGTTATTTGGGCTCAGAACTGCGAGCTGTCAGCTGGAACATTTCT 1069

421 ACAATAAATACCGGCTGTTATTTGGGCTCAGAACTGCGAGCTGTCAGCTGGAACATTTCT 480

1070 GTATTCATCTGCTATTTGTGATGCTCCGGGTGTTTCAACTAGAACCTTCAGACCCCAATGT 1129

481 GTATTCATCTGCTATTTGTGATGCTCCGGGTGTTTCAACTAGAACCTTCAGACCCCAATGT 540

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541 TATGAGAAACCTTAAAGAAATTTGAGGTTGAGAGTTTGTCCGAAATATCACAGTA 600

1190 GCGGTAGCTCAAGGATCAAGCTCCATCTCGTAACACCATCCAGAGTTTGTTCACGCA 1249

601 GCGGTAGCTCAAGGATCAAGCTCCATCTCGTAACACCATCCAGAGTTTGTTCACGCA 660

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721 TAAAGGATGAAGAGGAAACAGATGTCCTATTTGCTGTTGGGCGATGCTTCATGAAGAA 780

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781 GTCTTACAGTGTGGAAGACGGCTGCAGGAAACAGCTGCACCACTGCAATGTCATTTT 840

1430 GGGCAGAGAGTGTAGAGAAATAGAGAACTTTAATATGTCCTTGTAGATCTAAGT 1489

841 GGGCAGAGAGTGTAGAGAAATAGAGAACTTTAATATGTCCTTGTAGATCTAAGT 900

1490 GGAGATCTCATGATTTCTACAGCCACAGTGTGTAAGTCTGTGATTCCTCTTCTTCCC 1549

901 GGAGATCTCATGATTTCTACAGCCACAGTGTGTAAGTCTGTGATTCCTCTTCTTCCC 960

1550 TCAGAGCTGCAAGCAGCAAAACCGTACAGCAGCAGCTTTGGCTGGATCAAGAGGAATC 1609

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1790 TCTCTTGGCAATGGGAGAGCAGTGAATTTTGGGGGAGCAGTGGAGAGCAGCTTAA 1849

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1850 GTGGGGGAGCCACAGTGGCTTCTCCAGACAGTATCTCAGGAGATGTGTGGAGCAT 1909

1261 GCGCGGAGCGGCCAGCGGCTCTCCAGCCAGCATCTCAGGGGATGTGTGGAGCGT 1320

1910 GCTGAGCGTTCCTGTAATGCTGTGCTGAGCCCTCTACAAAGTGTACGTTGCTGTT 1969

1321 GCTGAGTGTCTGTCTATAGTCTGCGCTGACCCCTCTACAAAGTGTACGTTGCTGTT 1380

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1381 TAAACCAATTTAGAGCCATGCTGTATATACACTCTTGTCCACAGTCTGGCAGAAATCA 1440

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2210 ATTTGCTTAAATTTGATTTCTTGAACCAAACTGAATCAAACTTGGCAAGAACTTC 2269

1621 ATTTGCTTAAATTTGATTTCTTGAACCAAACTGAATCAAACTTGGCAAGAACTTC 1680

2270 TTGGCGCGCTTTGCTTATAGATAGTGTGTTTGGAAATTTCTGCTGTAATTTTATCTTC 2329

1681 TTGGCGCGCTTTGCTTATAGATAGTGTGTTTGGAAATTTCTGCTGTAATTTTATCTTC 1740

2330 ATATTTGCTAGTACTGATGTTTCCAGAGCTGAGCCCTGTTGAAATCAGGTATAGAGAGTGC 2389

1741 ATATTTGCTAGTACTGATGTTTCCAGAGCTGAGCCCTGTTGAAATCAGGTATAGAGAGTGC 1800

2390 TGTCCCTCTTAACTTTGCTTTGCAATGATTAATTTCCACTCAATGTTGGCAAC 2449

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2450 TTTCCAGAGGATCTACTTGAATTTGCAAGAACTGTTACTACAGTACCCATGTTGTTTT 2509

1861 TCTCTCGAGGATATATCTGAGCTCTGCGAGATGGTACCGCAGTCCCGCTGTTGTTTT 1920

2510 CAAAATGTTTGAAGATGCTGAGTGTTCAGTTCACCTTCCAGTTCACAGGATGCGTCCGC 2569

1921 CCAAGCTGTGTAACCACTGCTTAATGTTCTGCTGCTCCACCACTTCCAGGATGCGCGGC 1980

2570 GTTTGATGCTATTGCAAGATGAGTGGAAATTTGCCGAAGCCATCCAGTGTGGCGTGAAG 2629

QY

Db 1981 GTCTGATGGCTATCGCGATGAGGTAGAAATGCGGAGGTATCCAGCTGGGTGGAGG 2040  
QY 2630 ACATCTTGGATGGTCAACAGGACAGCTTCTTGCAGGCACTGTGTTCCCAACAACATATCTGG 2689  
Db 2041 ACATCTTGGATGGGCTATCAGGACAG---CTTACAGGCGCTGGCCCGCCAGCTGTCT-- 2095  
QY 2690 AAACACAGAGAACAGTTCCTCAGTGTCACAGTCCATTTAGAGAAACTGGAAAGGAT 2749  
Db 2096 -----AGAAAACAGCTCCCTTGAAGCACACAGTCCATAGAGAAACTGGAAAGGAC 2148  
QY 2750 TATGTGTACAAAATTGAGTGCCAGTTTCAGAGGACATTTCTGAGAGACTGGCCAGCATTT 2809  
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QY 2810 CAGTAGGACCTTCTAGTTCAACACACAAACAAACAAACAAACAAACAAACAAACAAACAA 2869  
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QY 2870 TGGTTCAAAACAAAGGACAGCCCAACAGTCAAGTCTTTGAACTCCTCTCTCTTTATCTCATC 2929  
Db 2254 CGGTTCAAAACAAAGGACAGCCCAACAGTCAAGTCTTTGAACTCCTCTCTCTTTATCTCATC 2310  
QY 2930 ATTCCCAATTAATGTTTCCAGCTTGTCAACCCCTTCTCTCTACCCGATCTGTACAG 2989  
Db 2311 ATGCTCAATTAATGTTTCCAGCAACATCAGCCCTTGTCTCTGCCCCCGTGTCTC--- 2367  
QY 2990 CTGCACTGCAACAGATCTCTTAAGCATAGACTTCAGGATTCATTCCTCTGAGATAC 3049  
Db 2368 -----CAGATATTCTTAAGCACACACCCAGGCAATTTGTTCCCTGCAAAATAC 2415  
QY 3050 CTTCTGCAATCTCTCAACACAGGCAAGTCTTCTTACATTTCCACAGAACTGTCTTG 3109  
Db 2416 CTTCCGCAATCTCTCAGACACAGGCAAGTCTCTCTACATTTCCAGGAACTGTCTTG 2475  
QY 3110 AAAACAAAGACTCAGATAAATTTCCTCCAGCTTTTACTCAGTCAAGACCTTGGCCCTCCA 3169  
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QY 3170 GTACATACAGGCAAGGCAATAGACCTACCCAGGTAATACAGTAAACAGGAG 3229  
Db 2536 GTACATACAGGCAAGGCAATAGACCTTCCCGGAGTACAGGCAAGTACAGG 2595  
QY 3230 ATCCCTCAAAAATAGCATGACATTTGATCTGACAGTGTTCGAATGTGATCAGACGT 3289  
Db 2596 ACGCCACAAAATAGCATGACATTTGATCTGGGAGTGTCTCAGGTGTGACAGAGCT 2655  
QY 3290 TTGGCTGTAGCAGCAATAGTAGTAATGCTGTATACCCAGTGAAGAGAGAGTGTACCC 3349  
Db 2656 TTGGCGGGCGGCAACAGTGGCAACGCGCTCATACCCAGGAGGAGACAGTGTTCACGC 2715  
QY 3350 CAGTAGAGAGAAATGCGAGATTAGATGTCATACAGAGCTCAACTCCAGATTAGGAGCC 3409  
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QY 3410 TTCTTTGAAGCACTATGCTTCAAGTGATACAAAGTAACATTTTAAAGTCAAGATGCTG 3469  
Db 2776 TTCTTTGAAGCATCCATGCTTCAAGTGATACAGAGTCACTTTCAAGTCCGAAAGTCCGCG 2835  
QY 3470 TCCTCTCTCTGAAAGGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3529  
Db 2836 TCCTCTCTCTGAAAGGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2895  
QY 3530 AAAAGTGCAAAAGAGAGATGGAAGCTGAAGAGAGAGAGATTTTATGCAATTTGCCATGGCAA 3589  
Db 2896 AAAAGTGCAAAAGAGATGGAAGCTGAAGAGAGAGAGATTTTATGCAATTTGCCATGGCAA 2955  
QY 3590 TGTACGCTCTCAGGATGCTTCCCATAGTTCCTCAGTGCAGGTTGAAAATGGAGAG 3649  
Db 2956 TGTACGCTCTCAGGATGCTTCCCATAGTTCCTCAGTGCAGGTTGAAAATGGAGAG 3015  
QY 3650 ATATCATCATTTTCAACAGGATACACAGAGACTCTTACAGGACATACCAAGCAAAAC 3709

Db 3016 ATATTATCATCATTCAGCAGGACACACAGAAACTCTTCCAGGACATACCAAGCGAAC 3075  
QY 3710 AACCTATAGAGAGACACTGAATGGCTGAAGGTCAAACAGATAGCCTTGGAGCATTTT 3769  
Db 3076 AGCCTTACAGAGAGACGCTGAGTGGCTGAAGGCGCAGACAGATGGCCCTGGAGCATTTT 3135  
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Db 3136 CTTCTTGTATCAGGCTCAAGATGCGGAACTGGAACTTTAATGGCTCTTAAACAGAGTGA 3195  
QY 3830 CTTATGTCAGAAACACATCTTCTGAGCAAGAGAGATGATAGAGCACTATAGAGAGAGA 3889  
Db 3196 CTTATGTCAGAAACACATCTTCTGAGCAAGAGAGATGATAGAGCACTATAGAGAGAGA 3255  
QY 3890 TAAAGATGATGAGCCATCTGAATCATCAAAACATCATTAGGATGTTGGAGCCAGCTGTG 3949  
Db 3256 TAAAGATGATGAGCCATCTGAATCATCAAAACATCATTAGGATGTTGGAGCCAGCTGTG 3315  
QY 3950 AGAAGAGCAATTTACAAATCTCTTCAATGATGAGTGGAGGGGGATCGGTGCTCATTTGC 4009  
Db 3316 AGAAGAGCAATTTACAAATCTCTTCAATGATGAGTGGAGGGGGATCGGTGCTCATTTGC 3375  
QY 4010 TCAGTAAATATGAGCCCTTCAAGAACTCAGTAGTTATTAACTACACTCAACAGTTACTCC 4069  
Db 3376 TCGTAAATATGAGCCCTTCAAGAACTCAGTAGTTATTAACTACACTCAACAGTTACTCC 3435  
QY 4070 GTGGCTTTCTGATCTCCATGAAAACCAATCATTTACAGAGATGTCAAGGTGCAATTT 4129  
Db 3436 GTGGCTTTCTGATCTCCATGAGAACCAAGATCATTTACAGAGATGTCAAGGTGCAATTT 3495  
QY 4130 TCGTAATGACAGCACTGCTCAGAGACTAAGAAATGACAGATTTTGGAGCTGCAGCCAGT 4189  
Db 3496 TCGTAATGACAGCACTGCTCAGAGCCGCTCAGAGCTGAGATTTGAGACTGCAGCCAGT 3555  
QY 4190 TGGCATCAAAAGAACTGCTCAGAGAGATTTTCAAGGCAATTTACTGGGCAATTTGCGAT 4249  
Db 3556 TGGCATCAAAAGAACTGCTCAGAGAGATTTTCAAGGCAATTTACTGGGCAATTTGCGAT 3615  
QY 4250 TTATGGCACTCAGGCTATGAGAGCTCAACAGATGAGAGGAGCTGTATGTATGGAGTG 4309  
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QY 4310 TTGGCTGTCTATTATAGAAATGGCTTTGTGCAAAACCCACCTTGGAAATGCAGAAACACT 4369  
Db 3676 TTGGCTGTCTATTATAGAAATGGCTTTGTGCAAAACCCACCTTGGAAATGCAGAAACACT 3735  
QY 4370 CCAATCATCTCTGCTTGAATTTAAGATGCTAGTGCAGACTACTCTCCATCGATCCCTT 4429  
Db 3736 CCAATCATCTCTGCTTGAATTTAAGATGCTAGTGCAGACTACTCTCCATCGATCCCTT 3795  
QY 4430 CCAATTTGCTCTCTGCTTGAATTTAAGATGCTAGTGCAGACTACTCTCCATCGATCCCTT 4489  
Db 3796 CCAATTTGCTCTCTGCTTGAATTTAAGATGCTAGTGCAGACTACTCTCCATCGATCCCTT 3855  
QY 4490 ACGAGCTCCATCAAGAGAGCTACTGAGAGCATCCAGTCTTCTGTAATCATAGGTAG 4545  
Db 3856 ACCGGCTCCGTCAGAGAGCTGCTGAAACATCCCGTCTTCCGTACCAAGCTGGTAG 3911

## RESULT 15

AAZ25069

ID AAZ25069 standard; cDNA; 3911 BP.

XX

AC AAZ25069;

XX

DT 09-DEC-1999 (first entry)

XX

DE Human MEK1 nucleotide sequence.

XX

KW MEK3; MEK2; MEK3; mitogen-activated protein kinase; MAPK; ERK; extracellular regulated kinase; signal transduction; regulation;

KW MAPK/ERK; MEK; MEK3; inflammation; cellular proliferation;

KW differentiation; development; cell death; ss.

```
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 3..3911
XX FT /*tag= a
XX FT /product= "MEK1"
XX PN WO9947686-A2.
XX XX
XX PD 23-SEP-1999.
XX XX
XX PF 15-MAR-1999; 99WO-US005556.
XX XX
XX PR 16-MAR-1998; 98US-0078153P.
XX PR 04-SEP-1998; 98US-0099165P.
XX XX
XX PA (CADU-) CADUS PHARM CORP.
XX XX
XX PI Johnson GL;
XX XX
XX DR WPI; 1999-571843/48.
XX DR P-PSDB; AY42104.
XX XX
XX PT New human MEK1 polynucleotides and polypeptides, used for regulating
XX PT signal transduction in cells.
XX XX
XX PS Claim 2; Fig 1; 159pp; English.
XX XX
XX CC The present sequence encodes human mitogen-activated protein kinase/
XX CC extracellular response kinase (MAPK/ERK) kinase kinase (MEKK),
XX CC specifically designated MEKK1. The MEKK proteins are used to modulate and
XX CC regulate signal transduction in cells, as well as for regulation of gene
XX CC transcription in a cell encoding MEKK, where the cell is involved in
XX CC inflammation, regulation of cellular proliferation and differentiation,
XX CC regulation of development, regulation of cell death or regulation of
XX CC inflammation. They are also used to prepare antibodies. MEKK
XX CC polynucleotides can be used to produce the protein recombinantly and as a
XX CC source of probes and primers
XX XX
XX SQ Sequence 3911 BP; 1058 A; 973 C; 975 G; 905 T; 0 U; 0 Other;

Query Match 62.7%; Score 3286.4; DB 2; Length 3911;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 3580; Conservative 0; Mismatches 331; Indels 45; Gaps 5;

QY 590 CAGCCTGGAAGCAGCAATGGTTGGAAAGAGAAATAGCGAGGCGCTGTGTGGTAAAC 649
DB 1 CGGCTGGAAGCAGCAGTGGTTGGAAGAGAAATAGCGAGGCGCTGTGTGGTAAAC 60
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QY 710 AGGTCCAGGCAAGTCGGCTTACCAGCTTCCAAAGGCGGACGAGTCTCTCTGCA 769
DB 121 AGGTCCAGGCAAGTCGGCTTACCAGCTTCCAAAGGCGGACGAGTCTCTCTGCA 180
QY 770 ACTCCCTCATGGTCCGACAGTGAATCAGAAATCAGAAATCCTCAGGAGTAAAGAGAAAAGATTT 829
DB 181 ACTCCCTCATGGTCCGACAGTGAATCAGAAATCAGAAATCCTCAGGAGTAAAGAGAAAAGATTT 240
QY 830 CCCAGATGCTTTTCAGAGTGCAGAAATCACACACCCGAGAGCCCTTCCAGATG 889
DB 241 CCCAGATGCTTTTCAGAGTGCAGAAATCACACACCCGAGAGCCCTTCCAGATG 300
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DB 301 GCTTCTCATTATAGCCCTCAGGAAACAAACCCGCGTGTAAACAAAGTATGGGGCCA 360
QY 950 GACTGTACTTACTGAGCAGATAGGGCTTACTCTTCTGATGGAGGAGACAGCCAG 1009
DB 361 GACTGTACTTACTGAGCAGATAGGGCTTACTCTTCTGATGGAGGAGACAGCCAG 420
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DB 421 ACAATAAATACCGGGTGTATTTATGGCCCTCAGAACTGCAGCTGTGCACGTGGAACATCT 480
QY 1070 GTATTCAATCTGCTATTTGTGATGCTCCGGGTGTTCCTCACTAGAACTTCCAGACCCATGT 1129
DB 481 GTATTCAATCTGCTATTTGTGATGCTCCGGGTGTTCCTCACTAGAACTTCCAGACCCATGT 540
QY 1130 TATGGAGAAAACCTTTAAAGAAATTTAGAGTTTGAGAGTTTGTTCAGAAATATCAGATTA 1189
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QY 1190 GCGTAGCTCAAGGATCAAGCTCCATCTCGTAAACCACTCAGAAAGTTTGTTCACGCA 1249
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DB 1321 GCTGCGAGTCTTCTGCTCAATGGTCTGTGCTGACCCCTGTCTACAAAGTGTAGTGTGCTT 1380
QY 1970 TAAAAACATTTAGAGCCATCTGTTATATATCTCTTGGCCACAGTTTTCAGGAAAGATCA 2029
DB 1381 TAAAAACATTTAGAGCCATCTGTTATATATCTCTTGGCCACAGTCTTGGCAGAAAGATCA 1440
QY 2030 AACTTCAGAGATCTTCCAGCCAGTGTGTAGACCACTCTCTTCCAGAGTCTGGCAGAAAGATCA 2089
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```



QY 2090 ATAGCGCAAGTCAGTGTCCATATCAACACTGTTGGAACTGTGCAGAGGCCAAGCAG 2149  
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DB 1561 GAAAGCTGGCGTTCGGGAGAGAAATACATAAAGCTGGTGTGTGTGTGTGTG 1620  
QY 2210 ATTATGCTTAAATGTTATCTTGGAAACCAAACTGAATCAAAATAAAGTGGCAAGATTC 2269  
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QY 2390 TGTCCCTCTTAACCTTTGCTTTCAGTCCATGATTAATTCCTCACTCAATGGTGGCAAC 2449  
DB 1801 TCTCCCTCTTAACCTTTGCTTTCAGTCCATGATTAATTCCTCACTCAATGGTGGCAAC 1860  
QY 2450 TTTCCAGAGGATCTACTTGTAGTTCCTGCAAGATGTTTACTACAGTACCCCATGTGTTTT 2509  
DB 1861 TCTCTCGGAGGATATCTGAGCTCTGCCAGATGTTGACCGAGTGCCTGCTGTGTTTT 1920  
QY 2510 CAARACTGTGAATGCTGAGTGTTCAGTTCCTCACTCACTTCCAGAGTGGTGGC 2569  
DB 1921 CCAAGCTGTAACCATGCTTAATGCTTCTGCTCCACCCTTCCAGAGTGGTGGC 1980  
QY 2570 GTTTGATGCTATTGTCAGATGAGTGGAAATGCGGAAGCCATCCAGTGGCGCTAGAAG 2629  
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DB 2096 -----AGAAACAGCTCCCTTGAGCACACAGTCCATAGAGAGAACTGGAAGGAC 2148  
QY 2750 TATGTGCTACAAATGAGTGCAGTTCAGAGGACATTTCTGAGAGTGGCCAGCATTT 2809  
DB 2149 TAAAGTCTACGAGTGTGAGTGCAGTTCGGAGGACATTTCTGACAGACTGGCGCGTCT 2208  
QY 2810 CAGTAGGACCTTCTAGTTCACAAACAAACAAACAAACAAACAGAGCAACCAAGCCAA 2869  
DB 2209 CTGTAGGACTTCCAGCT-----CAACAAACAGAGCAACCAAGCCAG 2253  
QY 2870 TGGTTCAACAAAGGAGAGACCCACAGTCAAGTGTGAACTCCTCTCTTTATCTCATC 2929  
DB 2254 CGGTTCAACAAAGGAGAGACCCACAGTCAAGTGTGAACTCCTCTCTCTTTTGTCTC -TC 2310  
QY 2930 ATTCCCAATTAATGTTTCCAGCTTGTCAACCCCTCTCTCTTACCCCATCTGTACCCAG 2989  
DB 2311 ATGCTCAATTAATGTTTCCAGCACCATCAGCCCTTGTCTCTGCCCCGTCTGTCTC - 2367  
QY 2990 CTGGCAGTGCACAGATGCTCTTAAGCATAGACTTCAGGAGTTCATTCCTCTGCAATAC 3049  
DB 2368 -----CAGATATTTCTAAGCACAGACCCCGAGCATTTGTTCCCTGCAAAATAC 2415  
QY 3050 CTTCTGCTCTCTCAACACAGCGCAAGTTCCTCACTCAATTCACAGAACTGCTCTG 3109  
DB 2416 CTTCTGCTCTCTCTCAACACAGCGCAAGTTCCTCACTCAATTCAGAGAACTGCTCTG 2475  
QY 3110 AAAACAAAGACTCAGATAAATTTCCCGAGTCTTTACTCAGTCAAGACCTTGGCCCTCA 3169  
DB 2476 AACACCGAGACTCAGACCGAGTCTCTCCAGTCTTCACTCAGTCAAGACCCCTCCA 2535  
QY 3170 GTAACATACACAGGCCAAGCCATCTAGACCTTACCCAGGTAAATACAGTAAACAGGAG 3229

DB 2536 GTAACATACACAGGCCAAGCCATCCGACCCGTTCCGGGAGTACAGCAAACTAGGGG 2595  
QY 3230 ATCCCTCTCAAAAATAGCATGACACTTGTATCTGAAACAGTAGTTCAAAATGTATGACAGCT 3289  
DB 2596 ACGCCACAAAATAGTACCATGACACTTGTATCTGGGAGTGTCTCCAGGTTGACAGAGCT 2655  
QY 3290 TTGGCTGTAGACGAATAGTAGTAAATGCTGTATTATACCCAGTGCACAGACAGTGTCAACC 3349  
DB 2656 TTGGCGCGCGCGCAACAGTGGCAACGCGCTCATACCCAGGACAGACAGTGTTCAGCG 2715  
QY 3350 CAGTAGAGAGAAATGCGAGATTAGATGTCAATACAGAGCTCAATCCAGTATTGAGGACC 3409  
DB 2716 CGGTGGAGGACAAAGTGCAGGTAGATGTGAACACCGAGCTCAACTCCAGCATCGAGGACC 2775  
QY 3410 TTCTTGAAGCATCTATGCTTCAAGCTTCAAGTAACTTTTAAAGTCAAGAGTGTCTG 3469  
DB 2776 TTCTTGAAGCATCTATGCTTCAAGTGAACAGACAGTCACTTTCAAGTCCGAAGTGGCG 2835  
QY 3470 TCTGTCTCTCTGAAAAGGCTGAAAATGATGATACCTACAAAGATGATGTGAATCATATC 3529  
DB 2836 TCTCTCTCTCGGAAAAGGCGGAAATGACGACACCTACAAAGACAGCTCAATCATATC 2895  
QY 3530 AAAAGTGAAGAGAGAAAGTGAAGCTGAAGAGAAAGAGCTTTAGCAATTTGCCATGGCA 3589  
DB 2896 AAAAGTGAAGAGAAAGTGAAGCTGAAGAGAGAGAGCTTTAGCGATCGCCATGGCA 2955  
QY 3590 TGTGAGCTCTCAGAGTGCCTCCCATAGTTCCTCAGCTGCAGGTGAAAAATGGAGAAG 3649  
DB 2956 TGTGAGCTCTCAGAGTGCCTCCCATAGTTCCTCAGCTGCAGGTGAAAAATGGAGAAG 3015  
QY 3650 ATATCATCATTTTCAACAGGATACACAGAGACTTACAGGACATACCAAGCAATACCAAGCAAAAC 3709  
DB 3016 ATATTCATCATTTCAACAGGATACACAGGACATACCAAGCAATACCAAGCAAAAC 3075  
QY 3710 AACCGTATAGAGAGACACTGATGCTGAAAGGCTCAACAGATAGGCTTTGAGAGCATTT 3769  
DB 3076 AGCCTTACAGAGAGAGCTGAGTGGCTGAAAGGCGCAGAGATAGGCTTCGAGAGCATTT 3135  
QY 3770 CTTCTTGTATTACAGCTCAAGATGTGGGAACTGGAACCTTTAATGCTGTTTAAACAGGTGA 3829  
DB 3136 CTTCTTGTATTACAGCTCAAGATGTGGGAACTGGAACCTTTAATGCTGTTTAAACAGGTGA 3195  
QY 3830 CTTATGTCAGAACACATCTCTGAGCAGAGAGAGTGTAGAACACTTAACAGAGAGAG 3889  
DB 3196 CTTATGTCAGAACACATCTCTGAGCAGAGAGAGTGTAGAACACTTAACAGAGAGAG 3255  
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DB 3256 TAAAGATGATGAGCCATCTGAATCTCAAAACATCATTTAGGATGTTGGAGAGCCAGTGTG 3315  
QY 3950 AGAGAGCAATTAACATCTCTTATGATGATGAGGAGGAGTGGGCTGCTATTCG 4009  
DB 3316 AGAGAGCAATTAACATCTCTTATGATGATGAGGAGGAGTGGGCTGCTATTCG 3375  
QY 4010 TGAAGTAAATATGAGGCTTCAAGAACTAGTATTATTAACCTACACTGAACTAGTACTCC 4069  
DB 3376 TGAAGTAAATATGAGGCTTCAAGAACTAGTATTATTAACCTACACTGAACTAGTACTCC 3435  
QY 4070 GTGGCTTTCTGATCTTCATGAAACCAATCATTCACAGAGATGTCAAGGTGCCAAT 4129  
DB 3436 GTGGCTTTCTGATCTTCATGAAACCAATCATTCACAGAGATGTCAAGGTGCCAAT 3495  
QY 4130 TGTAAATGACAGCACTGGTCAAGAGACTAAGAAATGCAATTTTGGAGCTGCAGCCAGGT 4189  
DB 3496 TGTCTATTGACAGCAGCTGAGAGCTGAGAAATGCAATTTGGAGCTGCAGCCAGGT 3555  
QY 4190 TGGCATCAAAAGGAACTGGTGCAGGAGAGTTCAGGGAACAATTACTGGGGACAATTTGAT 4249  
DB 3556 TGGCATCAAAAGGAACTGGTGCAGGAGAGTTCAGGGAACAATTACTGGGGACAATTTGAT 3615  
QY 4250 TTAGCACCTGAGGTACTTAAGAGGTCAACAGTATGGAAGGAGCTGTGATGTATGGAGTG 4309

Db 3616 TCATGGCGCTGAGTCTCTAAGAGGTGAGCAGTATGTTAGAGCTGTGATGTATGGAGTG 3675  
QY 4310 TTGCTGTGCTATTATAGAAATGGCTTGTGCAAAACCAACCATGGAATGCGAAAAACACT 4369  
Db 3676 TTGCTGCGCCATTATAGAAATGGCTTGTGCAAAACCAACCTTGGAAATGCAAAAAACACT 3735  
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QY 4430 CACATTTGCTCTCGTTTACGAGATGCGCTCTTGGTTGTTTAACTTCAACCTCAGG 4489  
Db 3796 CACACCTGTCCCTGGTTTACGAGATGCGCTCTTGGTTGTTTAACTTCAACCTCAGG 3855  
QY 4490 ACAGACCTCCATCAAGAGAGTACTGAAAGCTCCAGTCTTTCGTACTACATGGTAG 4545  
Db 3856 ACCGGCCTCCGTCAAGAGAGTGTGAACATCCGGTCTTCCGTACCAACGTGGTAG 3911

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